

SEQUENCE LISTING

<110> NOVAVAX, INC.
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 Glenn, Gregory
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<120> METHODS AND COMPOSITIONS FOR INDUCING IMMUNE RESPONSES AGAINST
 CLOSTRIDIUM DIFFICILE

<130> NOV-058/02W0

<150> US 62/474,434

<151> 2017-03-21

<150> US 62/471,636

<151> 2017-03-16

<160> 28

<170> PatentIn version 3.5

<210> 1

<211> 1813

<212> PRT

<213> Artificial Sequence

<220>

<223> Triple toxin vaccine BV1470

<220>

<221> misc_feature

<222> (588)..(588)

<223> Xaa can be any naturally occurring amino acid

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			20					25					30		

Ile	Lys	Asp	Gly	Asn	Leu	Lys	Phe	Glu	Glu	Lys	Lys	Val	Asp	Lys	Leu
		35					40					45			

Leu	Asp	Lys	Asp	Lys	Ser	Asp	Val	Lys	Ser	Ile	Arg	Trp	Thr	Gly	Arg
	50					55					60				

Ile Ile Pro Ser Lys Asp Gly Glu Tyr Thr Leu Ser Thr Asp Arg Asp
65 70 75 80

Asp Val Leu Met Gln Val Asn Thr Glu Ser Thr Ile Ser Asn Thr Leu
85 90 95

Lys Val Asn Met Lys Lys Gly Lys Glu Tyr Lys Val Arg Ile Glu Leu
100 105 110

Gln Asp Lys Asn Leu Gly Ser Ile Asp Asn Leu Ser Ser Pro Asn Leu
115 120 125

Tyr Trp Glu Leu Asp Gly Met Lys Lys Ile Ile Pro Glu Glu Asn Leu
130 135 140

Phe Leu Arg Asp Tyr Ser Asn Ile Glu Lys Asp Asp Pro Phe Ile Pro
145 150 155 160

Asn Asn Asn Phe Phe Asp Pro Lys Leu Met Ser Asp Trp Glu Asp Glu
165 170 175

Asp Leu Asp Thr Asp Asn Asp Asn Ile Pro Asp Ser Tyr Glu Arg Asn
180 185 190

Gly Tyr Thr Ile Lys Asp Leu Ile Ala Val Lys Trp Glu Asp Ser Phe
195 200 205

Ala Glu Gln Gly Tyr Lys Lys Tyr Val Ser Asn Tyr Leu Glu Ser Asn
210 215 220

Thr Ala Gly Asp Pro Tyr Thr Asp Tyr Glu Lys Ala Ser Gly Ser Phe
225 230 235 240

Asp Lys Ala Ile Lys Thr Glu Ala Arg Asp Pro Leu Val Ala Ala Tyr
245 250 255

Pro Ile Val Gly Val Gly Met Glu Lys Leu Ile Ile Ser Thr Asn Glu
260 265 270

His Ala Ser Thr Asp Gln Gly Lys Thr Val Ser Arg Ala Thr Thr Asn
275 280 285

Ser Lys Thr Glu Ser Asn Thr Ala Gly Val Ser Val Asn Val Gly Tyr
290 295 300

Gln Asn Gly Phe Thr Ala Asn Val Thr Thr Asn Tyr Ser His Thr Thr
305 310 315 320

Asp Asn Ser Thr Ala Val Gln Asp Ser Asn Gly Glu Ser Trp Asn Thr
325 330 335

Gly Leu Ser Ile Asn Lys Gly Glu Ser Ala Tyr Ile Asn Ala Asn Val
340 345 350

Arg Tyr Tyr Asn Thr Gly Thr Ala Pro Met Tyr Lys Val Thr Pro Thr
355 360 365

Thr Asn Leu Val Leu Asp Gly Asp Thr Leu Ser Thr Ile Lys Ala Gln
370 375 380

Glu Asn Gln Ile Gly Asn Asn Leu Ser Pro Gly Asp Thr Tyr Pro Lys
385 390 395 400

Lys Gly Leu Ser Pro Leu Ala Leu Asn Thr Met Asp Gln Phe Ser Ser
405 410 415

Arg Leu Ile Pro Ile Asn Tyr Asp Gln Leu Lys Lys Leu Asp Ala Gly
420 425 430

Lys Gln Ile Lys Leu Glu Thr Thr Gln Val Ser Gly Asn Phe Gly Thr
435 440 445

Lys Asn Ser Ser Gly Gln Ile Val Thr Glu Gly Asn Ser Trp Ser Asp
450 455 460

Tyr Ile Ser Gln Ile Asp Ser Ile Ser Ala Ser Ile Ile Leu Asp Thr
465 470 475 480

Glu Asn Glu Ser Tyr Glu Arg Arg Val Thr Ala Lys Asn Leu Gln Asp
485 490 495

Pro Glu Asp Lys Thr Pro Glu Leu Thr Ile Gly Glu Ala Ile Glu Lys
500 505 510

Ala Phe Gly Ala Thr Lys Lys Asp Gly Leu Leu Tyr Phe Asn Asp Ile
515 520 525

Pro Ile Asp Glu Ser Cys Val Glu Leu Ile Phe Asp Asp Asn Thr Ala
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Asn Lys Ile Lys Asp Ser Leu Lys Thr Leu Ser Asp Lys Lys Ile Tyr
545 550 555 560

Asn Val Lys Leu Glu Arg Gly Met Asn Ile Leu Ile Lys Thr Pro Thr
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Tyr Phe Thr Asn Phe Asp Asp Tyr Asn Asn Tyr Xaa Ser Thr Trp Ser
580 585 590

Asn Val Asn Thr Thr Asn Gln Asp Gly Leu Gln Gly Ser Ala Asn Lys
595 600 605

Leu Asn Gly Glu Thr Lys Ile Lys Ile Pro Met Ser Glu Leu Lys Pro
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Tyr Lys Arg Tyr Val Phe Ser Gly Tyr Ser Lys Asp Pro Leu Thr Ser
625 630 635 640

Asn Ser Ile Ile Val Lys Ile Lys Ala Lys Glu Glu Lys Thr Asp Tyr
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Leu Val Pro Glu Gln Gly Tyr Thr Lys Phe Ser Tyr Glu Phe Glu Thr
660 665 670

Thr Glu Lys Asp Ser Ser Asn Ile Glu Ile Thr Leu Ile Gly Ser Gly
675 680 685

Thr Thr Tyr Leu Asp Asn Leu Ser Ile Thr Glu Leu Asn Ser Thr Pro
690 695 700

Glu Ile Leu Asp Glu Pro Glu Val Lys Ile Pro Thr Asp Gln Glu Ile
705 710 715 720

Met Asp Ala His Lys Ile Tyr Phe Ala Asp Leu Asn Phe Asn Pro Ser
725 730 735

Thr Gly Asn Thr Tyr Ile Asn Gly Met Tyr Phe Ala Pro Thr Gln Thr
740 745 750

Asn Lys Glu Ala Leu Asp Tyr Ile Gln Lys Tyr Arg Val Glu Ala Thr
755 760 765

Leu Gln Tyr Ser Gly Phe Lys Asp Ile Gly Thr Lys Asp Lys Glu Met
770 775 780

Arg Asn Tyr Leu Gly Asp Pro Asn Gln Pro Lys Thr Asn Tyr Val Asn
785 790 795 800

Leu Arg Ser Tyr Phe Thr Gly Gly Glu Asn Ile Met Thr Tyr Lys Lys
805 810 815

Leu Arg Ile Tyr Ala Ile Thr Pro Asp Asp Arg Glu Leu Leu Val Leu
820 825 830

Ser Val Asp Ala Ser Met Val Ser Gly Leu Ile Tyr Ile Asn Asp Ser
835 840 845

Leu Tyr Tyr Phe Lys Pro Pro Val Asn Asn Leu Ile Thr Gly Phe Val
850 855 860

Thr Val Gly Asp Asp Lys Tyr Tyr Phe Asn Pro Ile Asn Gly Gly Ala
865 870 875 880

Ala Ser Ile Gly Glu Thr Ile Ile Asp Asp Lys Asn Tyr Tyr Phe Asn
885 890 895

Gln Ser Gly Val Leu Gln Thr Gly Val Phe Ser Thr Glu Asp Gly Phe
900 905 910

Lys Tyr Phe Ala Pro Ala Asn Thr Leu Asp Glu Asn Leu Glu Gly Glu
915 920 925

Ala Ile Asp Phe Thr Gly Lys Leu Ile Ile Asp Glu Asn Ile Tyr Tyr
930 935 940

Phe Asp Asp Asn Tyr Arg Gly Ala Val Glu Trp Lys Glu Leu Asp Gly
945 950 955 960

Glu Met His Tyr Phe Ser Pro Glu Thr Gly Lys Ala Phe Lys Gly Leu
965 970 975

Asn Gln Ile Gly Asp Tyr Lys Tyr Tyr Phe Asn Ser Asp Gly Val Met
980 985 990

Gln Lys Gly Phe Val Ser Ile Asn Asp Asn Lys His Tyr Phe Asp Asp
995 1000 1005

Ser Gly Val Met Lys Val Gly Tyr Thr Glu Ile Asp Gly Lys His
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Phe Tyr Phe Ala Glu Asn Gly Glu Met Gln Ile Gly Val Phe Asn
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Thr Glu Asp Gly Phe Lys Tyr Phe Ala His His Asn Glu Asp Leu
1040 1045 1050

Gly Asn Glu Glu Gly Glu Glu Ile Ser Tyr Ser Gly Ile Leu Asn
1055 1060 1065

Phe Asn Asn Lys Ile Tyr Tyr Phe Asp Asp Ser Phe Thr Ala Val
1070 1075 1080

Val Gly Trp Lys Asp Leu Glu Asp Gly Ser Lys Tyr Tyr Phe Asp
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Glu Asp Thr Ala Glu Ala Tyr Ile Gly Leu Ser Leu Ile Asn Asp
1100 1105 1110

Gly Gln Tyr Tyr Phe Asn Asp Asp Gly Ile Met Gln Val Gly Phe
1115 1120 1125

Val	Thr	Ile	Asn	Asp	Lys	Val	Phe	Tyr	Phe	Ser	Asp	Ser	Gly	Ile
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Ile	Glu	Ser	Gly	Val	Gln	Asn	Ile	Asp	Asp	Asn	Tyr	Phe	Tyr	Ile
1145						1150					1155			
Asp	Asp	Asn	Gly	Ile	Val	Gln	Ile	Gly	Val	Phe	Asp	Thr	Ser	Asp
1160						1165					1170			
Gly	Tyr	Lys	Tyr	Phe	Ala	Pro	Ala	Asn	Thr	Val	Asn	Asp	Asn	Ile
1175						1180					1185			
Tyr	Gly	Gln	Ala	Val	Glu	Tyr	Ser	Gly	Leu	Val	Arg	Val	Gly	Glu
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Asp	Val	Tyr	Tyr	Phe	Gly	Glu	Thr	Tyr	Thr	Ile	Glu	Thr	Gly	Trp
1205						1210					1215			
Ile	Tyr	Asp	Met	Glu	Asn	Glu	Ser	Asp	Lys	Tyr	Tyr	Phe	Asn	Pro
1220						1225					1230			
Glu	Thr	Lys	Lys	Ala	Cys	Lys	Gly	Ile	Asn	Leu	Ile	Asp	Asp	Ile
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Lys	Tyr	Tyr	Phe	Asp	Glu	Lys	Gly	Ile	Met	Arg	Thr	Gly	Leu	Ile
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Ser	Phe	Glu	Asn	Asn	Asn	Tyr	Tyr	Phe	Asn	Glu	Asn	Gly	Glu	Met
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Gln	Phe	Gly	Tyr	Ile	Asn	Ile	Glu	Asp	Lys	Met	Phe	Tyr	Phe	Gly
1280						1285					1290			
Glu	Asp	Gly	Val	Met	Gln	Ile	Gly	Val	Phe	Asn	Thr	Pro	Asp	Gly
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Phe	Lys	Tyr	Phe	Ala	His	Gln	Asn	Thr	Leu	Asp	Glu	Asn	Phe	Glu
1310						1315					1320			
Gly	Glu	Ser	Ile	Asn	Tyr	Thr	Gly	Trp	Leu	Asp	Leu	Asp	Glu	Lys
1325						1330					1335			

Arg Tyr Tyr Phe Thr Asp Glu Tyr Ile Ala Ala Thr Gly Ser Val
1340 1345 1350

Ile Ile Asp Gly Glu Glu Tyr Tyr Phe Asp Pro Asp Thr Ala Gln
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Leu Val Ile Ser Glu Ser Arg Met Val Thr Gly Val Phe Lys Gly
1370 1375 1380

Pro Asn Gly Phe Glu Tyr Phe Ala Pro Ala Asn Thr His Asn Asn
1385 1390 1395

Asn Ile Glu Gly Gln Ala Ile Val Tyr Gln Asn Lys Phe Leu Thr
1400 1405 1410

Leu Asn Gly Lys Lys Tyr Tyr Phe Asp Asn Asp Ser Lys Ala Val
1415 1420 1425

Thr Gly Trp Gln Thr Ile Asp Gly Lys Lys Tyr Tyr Phe Asn Leu
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Asn Thr Ala Glu Ala Ala Thr Gly Trp Gln Thr Ile Asp Gly Lys
1445 1450 1455

Lys Tyr Tyr Phe Asn Leu Asn Thr Ala Glu Ala Ala Thr Gly Trp
1460 1465 1470

Gln Thr Ile Asp Gly Lys Lys Tyr Tyr Phe Asn Thr Asn Thr Phe
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Ile Ala Ser Thr Gly Tyr Thr Ser Ile Asn Gly Lys His Phe Tyr
1490 1495 1500

Phe Asn Thr Asp Gly Ile Met Gln Ile Gly Val Phe Lys Gly Pro
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Asn Gly Phe Glu Tyr Phe Ala Pro Ala Asn Thr Asp Ala Asn Asn
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Ile Glu Gly Gln Ala Ile Leu Tyr Gln Asn Lys Phe Leu Thr Leu
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Asn Gly Lys Lys Tyr Tyr Phe Gly Ser Asp Ser Lys Ala Val Thr
1550 1555 1560

Gly Leu Arg Thr Ile Asp Gly Lys Lys Tyr Tyr Phe Asn Thr Asn
1565 1570 1575

Thr Ala Val Ala Val Thr Gly Trp Gln Thr Ile Asn Gly Lys Lys
1580 1585 1590

Tyr Tyr Phe Asn Thr Asn Thr Ser Ile Ala Ser Thr Gly Tyr Thr
1595 1600 1605

Ile Ile Ser Gly Lys His Phe Tyr Phe Asn Thr Asp Gly Ile Met
1610 1615 1620

Gln Ile Gly Val Phe Lys Gly Pro Asp Gly Phe Glu Tyr Phe Ala
1625 1630 1635

Pro Ala Asn Thr Asp Ala Asn Asn Ile Glu Gly Gln Ala Ile Arg
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Tyr Gln Asn Arg Phe Leu Tyr Leu His Asp Asn Ile Tyr Tyr Phe
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Gly Asn Asn Ser Lys Ala Ala Thr Gly Trp Val Thr Ile Asp Gly
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Asn Arg Tyr Tyr Phe Glu Pro Asn Thr Ala Met Gly Ala Asn Gly
1685 1690 1695

Tyr Lys Thr Ile Asp Asn Lys Asn Phe Tyr Phe Arg Asn Gly Leu
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Pro Gln Ile Gly Val Phe Lys Gly Ser Asn Gly Phe Glu Tyr Phe
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Ala Pro Ala Asn Thr Asp Ala Asn Asn Ile Glu Gly Gln Ala Ile
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Arg Tyr Gln Asn Arg Phe Leu His Leu Leu Gly Lys Ile Tyr Tyr
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Phe Gly Asn Asn Ser Lys Ala Val Thr Gly Trp Gln Thr Ile Asn
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Gly Lys Val Tyr Tyr Phe Met Pro Asp Thr Ala Met Ala Ala Ala
1775 1780 1785

Gly Gly Leu Phe Glu Ile Asp Gly Val Ile Tyr Phe Phe Gly Val
1790 1795 1800

Asp Gly Val Lys Ala Pro Gly Ile Tyr Gly Met Glu Ile Val Asn Glu
1805 1810 1 5

Asp Ile Leu Pro Asn Asn Gly Leu Met Gly Tyr Tyr Phe Thr Asp Glu
10 15 20

His Phe Lys Asp Leu Lys Leu Met Ala Pro Ile Lys Asp Gly Asn Leu
25 30 35

Lys Phe Glu Glu Lys Lys Val Asp Lys Leu Leu Asp Lys Asp Lys Ser
40 45 50

Asp Val Lys Ser Ile Arg Trp Thr Gly Arg Ile Ile Pro Ser Lys Asp
55 60 65 70

Gly Glu Tyr Thr Leu Ser Thr Asp Arg Asp Asp Val Leu Met Gln Val
75 80 85

Asn Thr Glu Ser Thr Ile Ser Asn Thr Leu Lys Val Asn Met Lys Lys
90 95 100

Gly Lys Glu Tyr Lys Val Arg Ile Glu Leu Gln Asp Lys Asn Leu Gly
105 110 115

Ser Ile Asp Asn Leu Ser Ser Pro Asn Leu Tyr Trp Glu Leu Asp Gly
120 125 130

Met Lys Lys Ile Ile Pro Glu Glu Asn Leu Phe Leu Arg Asp Tyr Ser
135 140 145 150

Asn Ile Glu Lys Asp Asp Pro Phe Ile Pro Asn Asn Asn Phe Phe Asp
155 160 165

Pro Lys Leu Met Ser Asp Trp Glu Asp Glu Asp Leu Asp Thr Asp Asn
170 175 180

Asp Asn Ile Pro Asp Ser Tyr Glu Arg Asn Gly Tyr Thr Ile Lys Asp
185 190 195

Leu Ile Ala Val Lys Trp Glu Asp Ser Phe Ala Glu Gln Gly Tyr Lys
200 205 210

Lys Tyr Val Ser Asn Tyr Leu Glu Ser Asn Thr Ala Gly Asp Pro Tyr
215 220 225 230

Thr Asp Tyr Glu Lys Ala Ser Gly Ser Phe Asp Lys Ala Ile Lys Thr
235 240 245

Glu Ala Arg Asp Pro Leu Val Ala Ala Tyr Pro Ile Val Gly Val Gly
250 255 260

Met Glu Lys Leu Ile Ile Ser Thr Asn Glu His Ala Ser Thr Asp Gln
265 270 275

Gly Lys Thr Val Ser Arg Ala Thr Thr Asn Ser Lys Thr Glu Ser Asn
280 285 290

Thr Ala Gly Val Ser Val Asn Val Gly Tyr Gln Asn Gly Phe Thr Ala
295 300 305 310

Asn Val Thr Thr Asn Tyr Ser His Thr Thr Asp Asn Ser Thr Ala Val
315 320 325

Gln Asp Ser Asn Gly Glu Ser Trp Asn Thr Gly Leu Ser Ile Asn Lys
330 335 340

Gly Glu Ser Ala Tyr Ile Asn Ala Asn Val Arg Tyr Tyr Asn Thr Gly
345 350 355

Thr Ala Pro Met Tyr Lys Val Thr Pro Thr Thr Asn Leu Val Leu Asp
360 365 370

Gly Asp Thr Leu Ser Thr Ile Lys Ala Gln Glu Asn Gln Ile Gly Asn
375 380 385 390

Asn Leu Ser Pro Gly Asp Thr Tyr Pro Lys Lys Gly Leu Ser Pro Leu
395 400 405

Ala Leu Asn Thr Met Asp Gln Phe Ser Ser Arg Leu Ile Pro Ile Asn
410 415 420

Tyr Asp Gln Leu Lys Lys Leu Asp Ala Gly Lys Gln Ile Lys Leu Glu
425 430 435

Thr Thr Gln Val Ser Gly Asn Phe Gly Thr Lys Asn Ser Ser Gly Gln
440 445 450

Ile Val Thr Glu Gly Asn Ser Trp Ser Asp Tyr Ile Ser Gln Ile Asp
455 460 465 470

Ser Ile Ser Ala Ser Ile Ile Leu Asp Thr Glu Asn Glu Ser Tyr Glu
475 480 485

Arg Arg Val Thr Ala Lys Asn Leu Gln Asp Pro Glu Asp Lys Thr Pro
490 495 500

Glu Leu Thr Ile Gly Glu Ala Ile Glu Lys Ala Phe Gly Ala Thr Lys
505 510 515

Lys Asp Gly Leu Leu Tyr Phe Asn Asp Ile Pro Ile Asp Glu Ser Cys
520 525 530

Val Glu Leu Ile Phe Asp Asp Asn Thr Ala Asn Lys Ile Lys Asp Ser
535 540 545 550

Leu Lys Thr Leu Ser Asp Lys Lys Ile Tyr Asn Val Lys Leu Glu Arg
555 560 565

Gly Met Asn Ile Leu Ile Lys Thr Pro Thr Tyr Phe Thr Asn Phe Asp
570 575 580

Asp Tyr Asn Asn Tyr Xaa Ser Thr Trp Ser Asn Val Asn Thr Thr Asn
585 590 595

Gln Asp Gly Leu Gln Gly Ser Ala Asn Lys Leu Asn Gly Glu Thr Lys
600 605 610

Ile Lys Ile Pro Met Ser Glu Leu Lys Pro Tyr Lys Arg Tyr Val Phe
615 620 625 630

Ser Gly Tyr Ser Lys Asp Pro Leu Thr Ser Asn Ser Ile Ile Val Lys
635 640 645

Ile Lys Ala Lys Glu Glu Lys Thr Asp Tyr Leu Val Pro Glu Gln Gly
650 655 660

Tyr Thr Lys Phe Ser Tyr Glu Phe Glu Thr Thr Glu Lys Asp Ser Ser
665 670 675

Asn Ile Glu Ile Thr Leu Ile Gly Ser Gly Thr Thr Tyr Leu Asp Asn
680 685 690

Leu Ser Ile Thr Glu Leu Asn Ser Thr Pro Glu Ile Leu Asp Glu Pro
695 700 705 710

Glu Val Lys Ile Pro Thr Asp Gln Glu Ile Met Asp Ala His Lys Ile
715 720 725

Tyr Phe Ala Asp Leu Asn Phe Asn Pro Ser Thr Gly Asn Thr Tyr Ile
730 735 740

Asn Gly Met Tyr Phe Ala Pro Thr Gln Thr Asn Lys Glu Ala Leu Asp
745 750 755

Tyr Ile Gln Lys Tyr Arg Val Glu Ala Thr Leu Gln Tyr Ser Gly Phe
760 765 770

Lys Asp Ile Gly Thr Lys Asp Lys Glu Met Arg Asn Tyr Leu Gly Asp
775 780 785 790

Pro Asn Gln Pro Lys Thr Asn Tyr Val Asn Leu Arg Ser Tyr Phe Thr
795 800 805

Gly Gly Glu Asn Ile Met Thr Tyr Lys Lys Leu Arg Ile Tyr Ala Ile
810 815 820

Thr Pro Asp Asp Arg Glu Leu Leu Val Leu Ser Val Asp Ala Ser Met
825 830 835

Val Ser Gly Leu Ile Tyr Ile Asn Asp Ser Leu Tyr Tyr Phe Lys Pro
840 845 850

Pro Val Asn Asn Leu Ile Thr Gly Phe Val Thr Val Gly Asp Asp Lys
855 860 865 870

Tyr Tyr Phe Asn Pro Ile Asn Gly Gly Ala Ala Ser Ile Gly Glu Thr
875 880 885

Ile Ile Asp Asp Lys Asn Tyr Tyr Phe Asn Gln Ser Gly Val Leu Gln
890 895 900

Thr Gly Val Phe Ser Thr Glu Asp Gly Phe Lys Tyr Phe Ala Pro Ala
905 910 915

Asn Thr Leu Asp Glu Asn Leu Glu Gly Glu Ala Ile Asp Phe Thr Gly
920 925 930

Lys Leu Ile Ile Asp Glu Asn Ile Tyr Tyr Phe Asp Asp Asn Tyr Arg
935 940 945 950

Gly Ala Val Glu Trp Lys Glu Leu Asp Gly Glu Met His Tyr Phe Ser
955 960 965

Pro Glu Thr Gly Lys Ala Phe Lys Gly Leu Asn Gln Ile Gly Asp Tyr
970 975 980

Lys Tyr Tyr Phe Asn Ser Asp Gly Val Met Gln Lys Gly Phe Val Ser
985 990 995

Ile Asn Asp Asn Lys His Tyr Phe Asp Asp Ser Gly Val Met Lys
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Val Gly Tyr Thr Glu Ile Asp Gly Lys His Phe Tyr Phe Ala Glu
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Asn Gly Glu Met Gln Ile Gly Val Phe Asn Thr Glu Asp Gly Phe
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Lys Tyr Phe Ala His His Asn Glu Asp Leu Gly Asn Glu Glu Gly
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Glu Glu Ile Ser Tyr Ser Gly Ile Leu Asn Phe Asn Asn Lys Ile
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Tyr Tyr Phe Asp Asp Ser Phe Thr Ala Val Val Gly Trp Lys Asp
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Leu Glu Asp Gly Ser Lys Tyr Tyr Phe Asp Glu Asp Thr Ala Glu
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Ala Tyr Ile Gly Leu Ser Leu Ile Asn Asp Gly Gln Tyr Tyr Phe
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Asn Asp Asp Gly Ile Met Gln Val Gly Phe Val Thr Ile Asn Asp
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Lys Val Phe Tyr Phe Ser Asp Ser Gly Ile Ile Glu Ser Gly Val
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Gln Asn Ile Asp Asp Asn Tyr Phe Tyr Ile Asp Asp Asn Gly Ile
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Val Gln Ile Gly Val Phe Asp Thr Ser Asp Gly Tyr Lys Tyr Phe
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Ala Pro Ala Asn Thr Val Asn Asp Asn Ile Tyr Gly Gln Ala Val
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Glu Tyr Ser Gly Leu Val Arg Val Gly Glu Asp Val Tyr Tyr Phe
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Gly Glu Thr Tyr Thr Ile Glu Thr Gly Trp Ile Tyr Asp Met Glu
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Asn Glu Ser Asp Lys Tyr Tyr Phe Asn Pro Glu Thr Lys Lys Ala
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Cys Lys Gly Ile Asn Leu Ile Asp Asp Ile Lys Tyr Tyr Phe Asp
1240 1245 1250

Glu Lys Gly Ile Met Arg Thr Gly Leu Ile Ser Phe Glu Asn Asn
1255 1260 1265

Asn Tyr Tyr Phe Asn Glu Asn Gly Glu Met Gln Phe Gly Tyr Ile
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Asn Ile Glu Asp Lys Met Phe Tyr Phe Gly Glu Asp Gly Val Met
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Gln Ile Gly Val Phe Asn Thr Pro Asp Gly Phe Lys Tyr Phe Ala
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His Gln Asn Thr Leu Asp Glu Asn Phe Glu Gly Glu Ser Ile Asn
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Tyr Thr Gly Trp Leu Asp Leu Asp Glu Lys Arg Tyr Tyr Phe Thr
1330 1335 1340

Asp Glu Tyr Ile Ala Ala Thr Gly Ser Val Ile Ile Asp Gly Glu
1345 1350 1355

Glu Tyr Tyr Phe Asp Pro Asp Thr Ala Gln Leu Val Ile Ser Glu
1360 1365 1370

Ser Arg Met Val Thr Gly Val Phe Lys Gly Pro Asn Gly Phe Glu
1375 1380 1385

Tyr Phe Ala Pro Ala Asn Thr His Asn Asn Asn Ile Glu Gly Gln
1390 1395 1400

Ala	Ile	Val	Tyr	Gln	Asn	Lys	Phe	Leu	Thr	Leu	Asn	Gly	Lys	Lys
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Tyr	Tyr	Phe	Asp	Asn	Asp	Ser	Lys	Ala	Val	Thr	Gly	Trp	Gln	Thr
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Ile	Asp	Gly	Lys	Lys	Tyr	Tyr	Phe	Asn	Leu	Asn	Thr	Ala	Glu	Ala
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Ala	Thr	Gly	Trp	Gln	Thr	Ile	Asp	Gly	Lys	Lys	Tyr	Tyr	Phe	Asn
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Leu	Asn	Thr	Ala	Glu	Ala	Ala	Thr	Gly	Trp	Gln	Thr	Ile	Asp	Gly
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Lys	Lys	Tyr	Tyr	Phe	Asn	Thr	Asn	Thr	Phe	Ile	Ala	Ser	Thr	Gly
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Tyr	Thr	Ser	Ile	Asn	Gly	Lys	His	Phe	Tyr	Phe	Asn	Thr	Asp	Gly
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Ile	Met	Gln	Ile	Gly	Val	Phe	Lys	Gly	Pro	Asn	Gly	Phe	Glu	Tyr
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Phe	Ala	Pro	Ala	Asn	Thr	Asp	Ala	Asn	Asn	Ile	Glu	Gly	Gln	Ala
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Ile	Leu	Tyr	Gln	Asn	Lys	Phe	Leu	Thr	Leu	Asn	Gly	Lys	Lys	Tyr
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Tyr	Phe	Gly	Ser	Asp	Ser	Lys	Ala	Val	Thr	Gly	Leu	Arg	Thr	Ile
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Asp	Gly	Lys	Lys	Tyr	Tyr	Phe	Asn	Thr	Asn	Thr	Ala	Val	Ala	Val
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Thr	Gly	Trp	Gln	Thr	Ile	Asn	Gly	Lys	Lys	Tyr	Tyr	Phe	Asn	Thr
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Asn	Thr	Ser	Ile	Ala	Ser	Thr	Gly	Tyr	Thr	Ile	Ile	Ser	Gly	Lys
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His Phe Tyr Phe Asn Thr Asp Gly Ile Met Gln Ile Gly Val Phe
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Lys Gly Pro Asp Gly Phe Glu Tyr Phe Ala Pro Ala Asn Thr Asp
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Ala Asn Asn Ile Glu Gly Gln Ala Ile Arg Tyr Gln Asn Arg Phe
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Leu Tyr Leu His Asp Asn Ile Tyr Tyr Phe Gly Asn Asn Ser Lys
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Ala Ala Thr Gly Trp Val Thr Ile Asp Gly Asn Arg Tyr Tyr Phe
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Glu Pro Asn Thr Ala Met Gly Ala Asn Gly Tyr Lys Thr Ile Asp
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Asn Lys Asn Phe Tyr Phe Arg Asn Gly Leu Pro Gln Ile Gly Val
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Phe Lys Gly Ser Asn Gly Phe Glu Tyr Phe Ala Pro Ala Asn Thr
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Asp Ala Asn Asn Ile Glu Gly Gln Ala Ile Arg Tyr Gln Asn Arg
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Phe Leu His Leu Leu Gly Lys Ile Tyr Tyr Phe Gly Asn Asn Ser
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Lys Ala Val Thr Gly Trp Gln Thr Ile Asn Gly Lys Val Tyr Tyr
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Phe Met Pro Asp Thr Ala Met Ala Ala Ala Gly Gly Leu Phe Glu
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Ile Asp Gly Val Ile Tyr Phe Phe Gly Val Asp Gly Val Lys Ala
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Pro Gly Ile Tyr Gly
1810

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<222> (588)..(588)
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35 40 45

Leu Asp Lys Asp Lys Ser Asp Val Lys Ser Ile Arg Trp Thr Gly Arg
50 55 60

Ile Ile Pro Ser Lys Asp Gly Glu Tyr Thr Leu Ser Thr Asp Arg Asp
65 70 75 80

Asp Val Leu Met Gln Val Asn Thr Glu Ser Thr Ile Ser Asn Thr Leu
85 90 95

Lys Val Asn Met Lys Lys Gly Lys Glu Tyr Lys Val Arg Ile Glu Leu
100 105 110

Gln Asp Lys Asn Leu Gly Ser Ile Asp Asn Leu Ser Ser Pro Asn Leu
115 120 125

Tyr Trp Glu Leu Asp Gly Met Lys Lys Ile Ile Pro Glu Glu Asn Leu
130 135 140

Phe Leu Arg Asp Tyr Ser Asn Ile Glu Lys Asp Asp Pro Phe Ile Pro

145		150		155		160									
Asn	Asn	Asn	Phe	Phe	Asp	Pro	Lys	Leu	Met	Ser	Asp	Trp	Glu	Asp	Glu
			165					170						175	
Asp	Leu	Asp	Thr	Asp	Asn	Asp	Asn	Ile	Pro	Asp	Ser	Tyr	Glu	Arg	Asn
			180					185					190		
Gly	Tyr	Thr	Ile	Lys	Asp	Leu	Ile	Ala	Val	Lys	Trp	Glu	Asp	Ser	Phe
		195					200					205			
Ala	Glu	Gln	Gly	Tyr	Lys	Lys	Tyr	Val	Ser	Asn	Tyr	Leu	Glu	Ser	Asn
	210					215					220				
Thr	Ala	Gly	Asp	Pro	Tyr	Thr	Asp	Tyr	Glu	Lys	Ala	Ser	Gly	Ser	Phe
225					230					235					240
Asp	Lys	Ala	Ile	Lys	Thr	Glu	Ala	Arg	Asp	Pro	Leu	Val	Ala	Ala	Tyr
				245					250					255	
Pro	Ile	Val	Gly	Val	Gly	Met	Glu	Lys	Leu	Ile	Ile	Ser	Thr	Asn	Glu
			260					265					270		
His	Ala	Ser	Thr	Asp	Gln	Gly	Lys	Thr	Val	Ser	Arg	Ala	Thr	Thr	Asn
	275						280					285			
Ser	Lys	Thr	Glu	Ser	Asn	Thr	Ala	Gly	Val	Ser	Val	Asn	Val	Gly	Tyr
	290					295					300				
Gln	Asn	Gly	Phe	Thr	Ala	Asn	Val	Thr	Thr	Asn	Tyr	Ser	His	Thr	Thr
305					310					315					320
Asp	Asn	Ser	Thr	Ala	Val	Gln	Asp	Ser	Asn	Gly	Glu	Ser	Trp	Asn	Thr
				325					330					335	
Gly	Leu	Ser	Ile	Asn	Lys	Gly	Glu	Ser	Ala	Tyr	Ile	Asn	Ala	Asn	Val
			340					345					350		
Arg	Tyr	Tyr	Asn	Thr	Gly	Thr	Ala	Pro	Met	Tyr	Lys	Val	Thr	Pro	Thr
		355					360					365			

Thr Asn Leu Val Leu Asp Gly Asp Thr Leu Ser Thr Ile Lys Ala Gln
370 375 380

Glu Asn Gln Ile Gly Asn Asn Leu Ser Pro Gly Asp Thr Tyr Pro Lys
385 390 395 400

Lys Gly Leu Ser Pro Leu Ala Leu Asn Thr Met Asp Gln Phe Ser Ser
405 410 415

Arg Leu Ile Pro Ile Asn Tyr Asp Gln Leu Lys Lys Leu Asp Ala Gly
420 425 430

Lys Gln Ile Lys Leu Glu Thr Thr Gln Val Ser Gly Asn Phe Gly Thr
435 440 445

Lys Asn Ser Ser Gly Gln Ile Val Thr Glu Gly Asn Ser Trp Ser Asp
450 455 460

Tyr Ile Ser Gln Ile Asp Ser Ile Ser Ala Ser Ile Ile Leu Asp Thr
465 470 475 480

Glu Asn Glu Ser Tyr Glu Arg Arg Val Thr Ala Lys Asn Leu Gln Asp
485 490 495

Pro Glu Asp Lys Thr Pro Glu Leu Thr Ile Gly Glu Ala Ile Glu Lys
500 505 510

Ala Phe Gly Ala Thr Lys Lys Asp Gly Leu Leu Tyr Phe Asn Asp Ile
515 520 525

Pro Ile Asp Glu Ser Cys Val Glu Leu Ile Phe Asp Asp Asn Thr Ala
530 535 540

Asn Lys Ile Lys Asp Ser Leu Lys Thr Leu Ser Asp Lys Lys Ile Tyr
545 550 555 560

Asn Val Lys Leu Glu Arg Gly Met Asn Ile Leu Ile Lys Thr Pro Thr
565 570 575

Tyr Phe Thr Asn Phe Asp Asp Tyr Asn Asn Tyr Xaa Ser Thr Trp Ser

580

585

590

Asn Val Asn Thr Thr Asn Gln Asp Gly Leu Gln Gly Ser Ala Asn Lys
 595 600 605

Leu Asn Gly Glu Thr Lys Ile Lys Ile Pro Met Ser Glu Leu Lys Pro
 610 615 620

Tyr Lys Arg Tyr Val Phe Ser Gly Tyr Ser Lys Asp Pro Leu Thr Ser
 625 630 635 640

Asn Ser Ile Ile Val Lys Ile Lys Ala Lys Glu Glu Lys Thr Asp Tyr
 645 650 655

Leu Val Pro Glu Gln Gly Tyr Thr Lys Phe Ser Tyr Glu Phe Glu Thr
 660 665 670

Thr Glu Lys Asp Ser Ser Asn Ile Glu Ile Thr Leu Ile Gly Ser Gly
 675 680 685

Thr Thr Tyr Leu Asp Asn Leu Ser Ile Thr Glu Leu Asn Ser Thr Pro
 690 695 700

Glu Ile Leu Asp Glu Pro Glu Val Lys Ile Pro Thr Asp Gln Glu Ile
 705 710 715 720

Met Asp Ala His Lys Ile Tyr Phe Ala Asp Leu Asn Phe Asn Pro Ser
 725 730 735

Thr Gly Asn Thr Tyr Ile Asn Gly Met Tyr Phe Ala Pro Thr Gln Thr
 740 745 750

Asn Lys Glu Ala Leu Asp Tyr Ile Gln Lys Tyr Arg Val Glu Ala Thr
 755 760 765

Leu Gln Tyr Ser Gly Phe Lys Asp Ile Gly Thr Lys Asp Lys Glu Met
 770 775 780

Arg Asn Tyr Leu Gly Asp Pro Asn Gln Pro Lys Thr Asn Tyr Val Asn
 785 790 795 800

Leu Arg Ser Tyr Phe Thr Gly Gly Glu Asn Ile Met Thr Tyr Lys Lys
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Leu Arg Ile Tyr Ala Ile Thr Pro Asp Asp Arg Glu Leu Leu Val Leu
820 825 830

Ser Val Asp
835

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<211> 536
<212> PRT
<213> Clostridium difficile

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Pro Pro Val Asn Asn Leu Ile Thr Gly Phe Val Thr Val Gly Asp Asp
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Lys Tyr Tyr Phe Asn Pro Ile Asn Gly Gly Ala Ala Ser Ile Gly Glu
35 40 45

Thr Ile Ile Asp Asp Lys Asn Tyr Tyr Phe Asn Gln Ser Gly Val Leu
50 55 60

Gln Thr Gly Val Phe Ser Thr Glu Asp Gly Phe Lys Tyr Phe Ala Pro
65 70 75 80

Ala Asn Thr Leu Asp Glu Asn Leu Glu Gly Glu Ala Ile Asp Phe Thr
85 90 95

Gly Lys Leu Ile Ile Asp Glu Asn Ile Tyr Tyr Phe Asp Asp Asn Tyr
100 105 110

Arg Gly Ala Val Glu Trp Lys Glu Leu Asp Gly Glu Met His Tyr Phe
115 120 125

Ser Pro Glu Thr Gly Lys Ala Phe Lys Gly Leu Asn Gln Ile Gly Asp
130 135 140

Tyr Lys Tyr Tyr Phe Asn Ser Asp Gly Val Met Gln Lys Gly Phe Val
145 150 155 160

Ser Ile Asn Asp Asn Lys His Tyr Phe Asp Asp Ser Gly Val Met Lys
165 170 175

Val Gly Tyr Thr Glu Ile Asp Gly Lys His Phe Tyr Phe Ala Glu Asn
180 185 190

Gly Glu Met Gln Ile Gly Val Phe Asn Thr Glu Asp Gly Phe Lys Tyr
195 200 205

Phe Ala His His Asn Glu Asp Leu Gly Asn Glu Glu Gly Glu Glu Ile
210 215 220

Ser Tyr Ser Gly Ile Leu Asn Phe Asn Asn Lys Ile Tyr Tyr Phe Asp
225 230 235 240

Asp Ser Phe Thr Ala Val Val Gly Trp Lys Asp Leu Glu Asp Gly Ser
245 250 255

Lys Tyr Tyr Phe Asp Glu Asp Thr Ala Glu Ala Tyr Ile Gly Leu Ser
260 265 270

Leu Ile Asn Asp Gly Gln Tyr Tyr Phe Asn Asp Asp Gly Ile Met Gln
275 280 285

Val Gly Phe Val Thr Ile Asn Asp Lys Val Phe Tyr Phe Ser Asp Ser
290 295 300

Gly Ile Ile Glu Ser Gly Val Gln Asn Ile Asp Asp Asn Tyr Phe Tyr
305 310 315 320

Ile Asp Asp Asn Gly Ile Val Gln Ile Gly Val Phe Asp Thr Ser Asp
325 330 335

Gly Tyr Lys Tyr Phe Ala Pro Ala Asn Thr Val Asn Asp Asn Ile Tyr
340 345 350

Gly Gln Ala Val Glu Tyr Ser Gly Leu Val Arg Val Gly Glu Asp Val
355 360 365

Tyr Tyr Phe Gly Glu Thr Tyr Thr Ile Glu Thr Gly Trp Ile Tyr Asp
370 375 380

Met Glu Asn Glu Ser Asp Lys Tyr Tyr Phe Asn Pro Glu Thr Lys Lys
385 390 395 400

Ala Cys Lys Gly Ile Asn Leu Ile Asp Asp Ile Lys Tyr Tyr Phe Asp
405 410 415

Glu Lys Gly Ile Met Arg Thr Gly Leu Ile Ser Phe Glu Asn Asn Asn
420 425 430

Tyr Tyr Phe Asn Glu Asn Gly Glu Met Gln Phe Gly Tyr Ile Asn Ile
435 440 445

Glu Asp Lys Met Phe Tyr Phe Gly Glu Asp Gly Val Met Gln Ile Gly
450 455 460

Val Phe Asn Thr Pro Asp Gly Phe Lys Tyr Phe Ala His Gln Asn Thr
465 470 475 480

Leu Asp Glu Asn Phe Glu Gly Glu Ser Ile Asn Tyr Thr Gly Trp Leu
485 490 495

Asp Leu Asp Glu Lys Arg Tyr Tyr Phe Thr Asp Glu Tyr Ile Ala Ala
500 505 510

Thr Gly Ser Val Ile Ile Asp Gly Glu Glu Tyr Tyr Phe Asp Pro Asp
515 520 525

Thr Ala Gln Leu Val Ile Ser Glu
530 535

<210> 4

<211> 438

<212> PRT

<213> Clostridium difficile

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Gln Asn Lys Phe Leu Thr Leu Asn Gly Lys Lys Tyr Tyr Phe Asp Asn
35 40 45

Asp Ser Lys Ala Val Thr Gly Trp Gln Thr Ile Asp Gly Lys Lys Tyr
50 55 60

Tyr Phe Asn Leu Asn Thr Ala Glu Ala Ala Thr Gly Trp Gln Thr Ile
65 70 75 80

Asp Gly Lys Lys Tyr Tyr Phe Asn Leu Asn Thr Ala Glu Ala Ala Thr
85 90 95

Gly Trp Gln Thr Ile Asp Gly Lys Lys Tyr Tyr Phe Asn Thr Asn Thr
100 105 110

Phe Ile Ala Ser Thr Gly Tyr Thr Ser Ile Asn Gly Lys His Phe Tyr
115 120 125

Phe Asn Thr Asp Gly Ile Met Gln Ile Gly Val Phe Lys Gly Pro Asn
130 135 140

Gly Phe Glu Tyr Phe Ala Pro Ala Asn Thr Asp Ala Asn Asn Ile Glu
145 150 155 160

Gly Gln Ala Ile Leu Tyr Gln Asn Lys Phe Leu Thr Leu Asn Gly Lys
165 170 175

Lys Tyr Tyr Phe Gly Ser Asp Ser Lys Ala Val Thr Gly Leu Arg Thr
180 185 190

Ile Asp Gly Lys Lys Tyr Tyr Phe Asn Thr Asn Thr Ala Val Ala Val
195 200 205

Thr Gly Trp Gln Thr Ile Asn Gly Lys Lys Tyr Tyr Phe Asn Thr Asn

210

215

220

Thr Ser Ile Ala Ser Thr Gly Tyr Thr Ile Ile Ser Gly Lys His Phe
 225 230 235 240

Tyr Phe Asn Thr Asp Gly Ile Met Gln Ile Gly Val Phe Lys Gly Pro
 245 250 255

Asp Gly Phe Glu Tyr Phe Ala Pro Ala Asn Thr Asp Ala Asn Asn Ile
 260 265 270

Glu Gly Gln Ala Ile Arg Tyr Gln Asn Arg Phe Leu Tyr Leu His Asp
 275 280 285

Asn Ile Tyr Tyr Phe Gly Asn Asn Ser Lys Ala Ala Thr Gly Trp Val
 290 295 300

Thr Ile Asp Gly Asn Arg Tyr Tyr Phe Glu Pro Asn Thr Ala Met Gly
 305 310 315 320

Ala Asn Gly Tyr Lys Thr Ile Asp Asn Lys Asn Phe Tyr Phe Arg Asn
 325 330 335

Gly Leu Pro Gln Ile Gly Val Phe Lys Gly Ser Asn Gly Phe Glu Tyr
 340 345 350

Phe Ala Pro Ala Asn Thr Asp Ala Asn Asn Ile Glu Gly Gln Ala Ile
 355 360 365

Arg Tyr Gln Asn Arg Phe Leu His Leu Leu Gly Lys Ile Tyr Tyr Phe
 370 375 380

Gly Asn Asn Ser Lys Ala Val Thr Gly Trp Gln Thr Ile Asn Gly Lys
 385 390 395 400

Val Tyr Tyr Phe Met Pro Asp Thr Ala Met Ala Ala Ala Gly Gly Leu
 405 410 415

Phe Glu Ile Asp Gly Val Ile Tyr Phe Phe Gly Val Asp Gly Val Lys
 420 425 430

Ala Pro Gly Ile Tyr Gly
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<220>
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 <211> 2505
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 <213> Clostridium difficile

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 <223> n is a, c, g, or t

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atggacgctc acaagatcta cttcgccgac ctgaacttca acccctctac tggaacaca	2220
tacatcaacg gcatgtactt cgctcctaca caaaccaaca aggaggccct ggactacatc	2280
cagaagtacc gtgtcgaagc cactctcaa tactccggtt tcaaggatat cggcacaag	2340
gacaaggaga tgaggaacta cttgggtgac ccaaaccagc cgaagaccaa ctacgtgaac	2400
ctgagatcat acttcactgg tggcgagaac atcatgacat acaagaagct gcgtatctac	2460
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<210> 7
 <211> 1608
 <212> DNA
 <213> Clostridium difficile

<400> 7	
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ggtggcgctg cctccatcgg cgagaccatc atcgacgata agaactacta cttcaaccag	180
agcggagttc tccaaactgg tgtgttctca acagaggacg gtttcaagta cttcgctccg	240
gccaacacct tggacgaaaa cctggagggt gaagccatcg acttcactgg caagttgatc	300
atcgatgaga acatctacta cttcgacgat aactaccgcg gtgctgtgga gtggaaggaa	360
ctcgacggcg agatgcacta cttctctcca gaaaccggca aggccttcaa gggattgaac	420
cagatcgggtg actacaagta ctacttcaac tcggatggcg tgatgcaaaa gggattcgtc	480
tccatcaacg acaacaagca ctacttcgac gattccggtg ttatgaaagt gggctacaca	540

gagatcgacg gcaagcactt ctacttcgct gagaacggag aaatgcagat cggtgtcttc	600
aacactgaag atggtttcaa gtacttcgcc caccacaacg aagatttggg caacgaggaa	660
ggagaggaaa tcagctactc aggcacacctg aacttcaaca acaagatcta ctacttcgat	720
gactctttca ccgctgtggt cggatggaag gacctggagg atggtagcaa gtactacttc	780
gacgaggata ctgctgaagc ctacatcggc ctgtcgtca tcaacgacgg acagtactac	840
ttcaacgacg atggcatcat gcaagtcgga ttcgttacca tcaacgacaa ggtgttctac	900
ttctcggatt ccggtatcat cgagtctggc gtccagaaca tcgacgataa ctacttctac	960
atcgacgata acggaatcgt gcaaatcggg gtcttcgaca caagcgatgg ctacaagtac	1020
ttcgctcccg ccaacaccgt gaacgacaac atctacggac aggctgtgga gtactcaggc	1080
ctgggtccgtg ttggagaaga cgtgtactac ttggcgaga cctacactat cgaaactgga	1140
tggatctacg acatggagaa cgaatctgac aagtactact tcaaccctga gacaaagaag	1200
gcctgcaagg gtatcaacct gatcgacgat atcaagtact acttcgatga aaagggtatc	1260
atgcgaccg gcctcatctc attcgaaac aacaactact acttcaacga gaacggagaa	1320
atgcaattcg gttacatcaa catcgaggac aagatgttct acttcggaga agatggtgtc	1380
atgcagatcg gtgttttcaa cactccagac ggcttcaagt acttcgctca ccaaacaca	1440
ctcgacgaga acttcgaggg agaatccatc aactacactg gttggttgga cctggatgag	1500
aagaggtact acttcaccga cgaatacatc gctgccactg gctccgtcat catcgacgga	1560
gaggaatact acttcgaccc ggatacagcc cagctggtca tctctgaa	1608

<210> 8
 <211> 1317
 <212> DNA
 <213> Clostridium difficile

<400> 8	
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ggcaagaagt attattttga caacgattct aaggccgtta ctggctggca aacaatcgac	180
ggaaagaagt attatttcaa tctgaacact gccgaggctg ccaccggttg gcagactatc	240
gatggcaaga agtactactt taacctcaac actgccgaag ctgccacagg atggcaaacc	300
atcgacggca agaagtacta ttttaacaca aacaccttca tcgcttctac tggctacaca	360

agcatcaacg gaaagcattt ttatttcaac accgatggaa tcatgcagat cgggtgtgttc	420
aagggaccaa acggtttcga atacttcgct ccggctaaca cagacgctaa caacatcgag	480
ggccaggcta tcttgtacca aaacaagttc ctcactttga acggcaagaa gtactatttt	540
ggctctgaca gcaaggccgt cactggactg aggacaatcg atggcaagaa gtactacttt	600
aatactaaca cagccgttgc tgtgaccggc tggcagacta tcaacggaaa gaagtattat	660
ttcaatacca acacttcaat cgcttcgacc ggttacacta tcattctctgg caagcatttt	720
tattttaaca ccgacggcat catgcaaadc ggtgtcttca agggccccga tggcttcgaa	780
tacttcgccc ccgctaacac tgatgctaac aacatcgagg gacaggctat ccgttaccaa	840
aaccgcttcc tgtacctcca cgacaacatc tactacttcg gcaacaactc aaaggctgcc	900
acaggatggg tgaccatcga tggtaaccgt tactacttcg agcccaacac tgccatgggt	960
gctaacggct acaagacaat cgacaacaag aacttctact tccgcaacgg tctcccacag	1020
atcggcgtct tcaagggatc aaacggtttc gactacttcg ctcttgccaa caccgacgcc	1080
aacaacatcg agggccaagc tatcaggtac caaacagat tcctgcacct gctcggcaag	1140
atctactact tcggaaacaa ctcgaaggcc gttactgggt ggagacaat caacggcaag	1200
gtgtactact tcatgccaga caccgctatg gctgccgctg gtggcctctt cgaaatcgac	1260
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<210> 9
 <211> 1820
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Triple toxin vaccine BV1420

<220>
 <221> misc_feature
 <222> (595)..(595)
 <223> Xaa can be any naturally occurring amino acid

<400> 9

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Tyr Tyr Phe Thr Asp Glu His Phe Lys Asp Leu Lys Leu Met Ala Pro
20 25 30

Ile Lys Asp Gly Asn Leu Lys Phe Glu Glu Lys Lys Val Asp Lys Leu
35 40 45

Leu Asp Lys Asp Lys Ser Asp Val Lys Ser Ile Arg Trp Thr Gly Arg
50 55 60

Ile Ile Pro Ser Lys Asp Gly Glu Tyr Thr Leu Ser Thr Asp Arg Asp
65 70 75 80

Asp Val Leu Met Gln Val Asn Thr Glu Ser Thr Ile Ser Asn Thr Leu
85 90 95

Lys Val Asn Met Lys Lys Gly Lys Glu Tyr Lys Val Arg Ile Glu Leu
100 105 110

Gln Asp Lys Asn Leu Gly Ser Ile Asp Asn Leu Ser Ser Pro Asn Leu
115 120 125

Tyr Trp Glu Leu Asp Gly Met Lys Lys Ile Ile Pro Glu Glu Asn Leu
130 135 140

Phe Leu Arg Asp Tyr Ser Asn Ile Glu Lys Asp Asp Pro Phe Ile Pro
145 150 155 160

Asn Asn Asn Phe Phe Asp Pro Lys Leu Arg Ala Arg Arg Arg Lys Lys
165 170 175

Arg Met Ser Asp Trp Glu Asp Glu Asp Leu Asp Thr Asp Asn Asp Asn
180 185 190

Ile Pro Asp Ser Tyr Glu Arg Asn Gly Tyr Thr Ile Lys Asp Leu Ile
195 200 205

Ala Val Lys Trp Glu Asp Ser Phe Ala Glu Gln Gly Tyr Lys Lys Tyr
210 215 220

Val Ser Asn Tyr Leu Glu Ser Asn Thr Ala Gly Asp Pro Tyr Asp Tyr
225 230 235 240

Glu Lys Ala Ser Gly Ser Phe Asp Lys Ala Ile Lys Thr Glu Ala Arg
245 250 255

Asp Pro Leu Val Ala Ala Tyr Pro Ile Val Gly Val Gly Met Glu Lys
260 265 270

Leu Ile Ile Ser Thr Asn Glu His Ala Ser Thr Asp Gln Gly Lys Thr
275 280 285

Val Ser Arg Ala Thr Thr Asn Ser Lys Thr Glu Ser Asn Thr Ala Gly
290 295 300

Val Ser Val Asn Val Gly Tyr Gln Asn Gly Phe Thr Ala Asn Val Thr
305 310 315 320

Thr Asn Tyr Ser His Thr Thr Asp Asn Ser Thr Ala Val Gln Asp Ser
325 330 335

Asn Gly Glu Ser Trp Asn Thr Gly Leu Ser Ile Asn Lys Gly Glu Ser
340 345 350

Ala Tyr Ile Asn Ala Asn Val Arg Tyr Tyr Asn Thr Gly Thr Ala Pro
355 360 365

Met Tyr Lys Val Thr Pro Thr Thr Asn Leu Val Leu Asp Gly Asp Thr
370 375 380

Leu Ser Thr Ile Lys Ala Gln Glu Asn Gln Ile Gly Asn Asn Leu Ser
385 390 395 400

Pro Gly Asp Thr Tyr Pro Lys Lys Gly Leu Ser Pro Leu Ala Leu Asn
405 410 415

Thr Met Asp Gln Phe Ser Ser Arg Leu Ile Pro Ile Asn Tyr Asp Gln
420 425 430

Leu Lys Lys Leu Asp Ala Gly Lys Gln Ile Lys Leu Glu Thr Thr Gln
435 440 445

Val Ser Gly Asn Phe Gly Thr Lys Asn Ser Ser Gly Gln Ile Val Thr
450 455 460

Glu Gly Asn Ser Trp Ser Asp Tyr Ile Ser Gln Ile Asp Ser Ile Ser
465 470 475 480

Ala Ser Ile Ile Leu Asp Thr Glu Asn Glu Ser Tyr Glu Arg Arg Val
485 490 495

Thr Ala Lys Asn Leu Gln Asp Pro Glu Asp Lys Thr Pro Glu Leu Thr
500 505 510

Ile Gly Glu Ala Ile Glu Lys Ala Phe Gly Ala Thr Lys Lys Asp Gly
515 520 525

Leu Leu Tyr Phe Asn Asp Ile Pro Ile Asp Glu Ser Cys Val Glu Leu
530 535 540

Ile Phe Asp Asp Asn Thr Ala Asn Lys Ile Lys Asp Ser Leu Lys Thr
545 550 555 560

Leu Ser Asp Lys Lys Ile Tyr Asn Val Lys Leu Glu Arg Gly Met Asn
565 570 575

Ile Leu Ile Lys Thr Pro Thr Tyr Phe Thr Asn Phe Asp Asp Tyr Asn
580 585 590

Asn Tyr Xaa Ser Thr Trp Ser Asn Val Asn Thr Thr Asn Gln Asp Gly
595 600 605

Leu Gln Gly Ser Ala Asn Lys Leu Asn Gly Glu Thr Lys Ile Lys Ile
610 615 620

Pro Met Ser Glu Leu Lys Pro Tyr Lys Arg Tyr Val Phe Ser Gly Tyr
625 630 635 640

Ser Lys Asp Pro Leu Thr Ser Asn Ser Ile Ile Val Lys Ile Lys Ala
645 650 655

Lys Glu Glu Lys Thr Asp Tyr Leu Val Pro Glu Gln Gly Tyr Thr Lys
660 665 670

Phe Ser Tyr Glu Phe Glu Thr Thr Glu Lys Asp Ser Ser Asn Ile Glu
675 680 685

Ile Thr Leu Ile Gly Ser Gly Thr Thr Tyr Leu Asp Asn Leu Ser Ile
690 695 700

Thr Glu Leu Asn Ser Thr Pro Glu Ile Leu Asp Glu Pro Glu Val Lys
705 710 715 720

Ile Pro Thr Asp Gln Glu Ile Met Asp Ala His Lys Ile Tyr Phe Ala
725 730 735

Asp Leu Asn Phe Asn Pro Ser Thr Gly Asn Thr Tyr Ile Asn Gly Met
740 745 750

Tyr Phe Ala Pro Thr Gln Thr Asn Lys Glu Ala Leu Asp Tyr Ile Gln
755 760 765

Lys Tyr Arg Val Glu Ala Thr Leu Gln Tyr Ser Gly Phe Lys Asp Ile
770 775 780

Gly Thr Lys Asp Lys Glu Met Arg Asn Tyr Leu Gly Asp Pro Asn Gln
785 790 795 800

Pro Lys Thr Asn Tyr Val Asn Leu Arg Ser Tyr Phe Thr Gly Gly Glu
805 810 815

Asn Ile Met Thr Tyr Lys Lys Leu Arg Ile Tyr Ala Ile Thr Pro Asp
820 825 830

Asp Arg Glu Leu Leu Val Leu Ser Val Asp Ala Ser Met Val Ser Gly
835 840 845

Leu Ile Tyr Ile Asn Asp Ser Leu Tyr Tyr Phe Lys Pro Pro Val Asn
850 855 860

Asn Leu Ile Thr Gly Phe Val Thr Val Gly Asp Asp Lys Tyr Tyr Phe
865 870 875 880

Asn Pro Ile Asn Gly Gly Ala Ala Ser Ile Gly Glu Thr Ile Ile Asp
885 890 895

Asp Lys Asn Tyr Tyr Phe Asn Gln Ser Gly Val Leu Gln Thr Gly Val
900 905 910

Phe Ser Thr Glu Asp Gly Phe Lys Tyr Phe Ala Pro Ala Asn Thr Leu
915 920 925

Asp Glu Asn Leu Glu Gly Glu Ala Ile Asp Phe Thr Gly Lys Leu Ile
930 935 940

Ile Asp Glu Asn Ile Tyr Tyr Phe Asp Asp Asn Tyr Arg Gly Ala Val
945 950 955 960

Glu Trp Lys Glu Leu Asp Gly Glu Met His Tyr Phe Ser Pro Glu Thr
965 970 975

Gly Lys Ala Phe Lys Gly Leu Asn Gln Ile Gly Asp Tyr Lys Tyr Tyr
980 985 990

Phe Asn Ser Asp Gly Val Met Gln Lys Gly Phe Val Ser Ile Asn Asp
995 1000 1005

Asn Lys His Tyr Phe Asp Asp Ser Gly Val Met Lys Val Gly Tyr
1010 1015 1020

Thr Glu Ile Asp Gly Lys His Phe Tyr Phe Ala Glu Asn Gly Glu
1025 1030 1035

Met Gln Ile Gly Val Phe Asn Thr Glu Asp Gly Phe Lys Tyr Phe
1040 1045 1050

Ala His His Asn Glu Asp Leu Gly Asn Glu Glu Gly Glu Glu Ile
1055 1060 1065

Ser Tyr Ser Gly Ile Leu Asn Phe Asn Asn Lys Ile Tyr Tyr Phe
1070 1075 1080

Asp Asp Ser Phe Thr Ala Val Val Gly Trp Lys Asp Leu Glu Asp
1085 1090 1095

Gly Ser Lys Tyr Tyr Phe Asp Glu Asp Thr Ala Glu Ala Tyr Ile
1100 1105 1110

Gly Leu Ser Leu Ile Asn Asp Gly Gln Tyr Tyr Phe Asn Asp Asp
1115 1120 1125

Gly Ile Met Gln Val Gly Phe Val Thr Ile Asn Asp Lys Val Phe
1130 1135 1140

Tyr Phe Ser Asp Ser Gly Ile Ile Glu Ser Gly Val Gln Asn Ile
1145 1150 1155

Asp Asp Asn Tyr Phe Tyr Ile Asp Asp Asn Gly Ile Val Gln Ile
1160 1165 1170

Gly Val Phe Asp Thr Ser Asp Gly Tyr Lys Tyr Phe Ala Pro Ala
1175 1180 1185

Asn Thr Val Asn Asp Asn Ile Tyr Gly Gln Ala Val Glu Tyr Ser
1190 1195 1200

Gly Leu Val Arg Val Gly Glu Asp Val Tyr Tyr Phe Gly Glu Thr
1205 1210 1215

Tyr Thr Ile Glu Thr Gly Trp Ile Tyr Asp Met Glu Asn Glu Ser
1220 1225 1230

Asp Lys Tyr Tyr Phe Asn Pro Glu Thr Lys Lys Ala Cys Lys Gly
1235 1240 1245

Ile Asn Leu Ile Asp Asp Ile Lys Tyr Tyr Phe Asp Glu Lys Gly
1250 1255 1260

Ile Met Arg Thr Gly Leu Ile Ser Phe Glu Asn Asn Asn Tyr Tyr
1265 1270 1275

Phe Asn Glu Asn Gly Glu Met Gln Phe Gly Tyr Ile Asn Ile Glu
1280 1285 1290

Asp Lys Met Phe Tyr Phe Gly Glu Asp Gly Val Met Gln Ile Gly
1295 1300 1305

Val Phe Asn Thr Pro Asp Gly Phe Lys Tyr Phe Ala His Gln Asn
1310 1315 1320

Thr Leu Asp Glu Asn Phe Glu Gly Glu Ser Ile Asn Tyr Thr Gly
1325 1330 1335

Trp Leu Asp Leu Asp Glu Lys Arg Tyr Tyr Phe Thr Asp Glu Tyr
1340 1345 1350

Ile Ala Ala Thr Gly Ser Val Ile Ile Asp Gly Glu Glu Tyr Tyr
1355 1360 1365

Phe Asp Pro Asp Thr Ala Gln Leu Val Ile Ser Glu Ser Arg Met
1370 1375 1380

Val Thr Gly Val Phe Lys Gly Pro Asn Gly Phe Glu Tyr Phe Ala
1385 1390 1395

Pro Ala Asn Thr His Asn Asn Asn Ile Glu Gly Gln Ala Ile Val
1400 1405 1410

Tyr Gln Asn Lys Phe Leu Thr Leu Asn Gly Lys Lys Tyr Tyr Phe
1415 1420 1425

Asp Asn Asp Ser Lys Ala Val Thr Gly Trp Gln Thr Ile Asp Gly
1430 1435 1440

Lys Lys Tyr Tyr Phe Asn Leu Asn Thr Ala Glu Ala Ala Thr Gly
1445 1450 1455

Trp Gln Thr Ile Asp Gly Lys Lys Tyr Tyr Phe Asn Leu Asn Thr
1460 1465 1470

Ala Glu Ala Ala Thr Gly Trp Gln Thr Ile Asp Gly Lys Lys Tyr
1475 1480 1485

Tyr Phe Asn Thr Asn Thr Phe Ile Ala Ser Thr Gly Tyr Thr Ser
1490 1495 1500

Ile Asn Gly Lys His Phe Tyr Phe Asn Thr Asp Gly Ile Met Gln
1505 1510 1515

Ile Gly Val Phe Lys Gly Pro Asn Gly Phe Glu Tyr Phe Ala Pro
1520 1525 1530

Ala Asn Thr Asp Ala Asn Asn Ile Glu Gly Gln Ala Ile Leu Tyr
1535 1540 1545

Gln Asn Lys Phe Leu Thr Leu Asn Gly Lys Lys Tyr Tyr Phe Gly
1550 1555 1560

Ser Asp Ser Lys Ala Val Thr Gly Leu Arg Thr Ile Asp Gly Lys
1565 1570 1575

Lys Tyr Tyr Phe Asn Thr Asn Thr Ala Val Ala Val Thr Gly Trp
1580 1585 1590

Gln Thr Ile Asn Gly Lys Lys Tyr Tyr Phe Asn Thr Asn Thr Ser
1595 1600 1605

Ile Ala Ser Thr Gly Tyr Thr Ile Ile Ser Gly Lys His Phe Tyr
1610 1615 1620

Phe Asn Thr Asp Gly Ile Met Gln Ile Gly Val Phe Lys Gly Pro
1625 1630 1635

Asp Gly Phe Glu Tyr Phe Ala Pro Ala Asn Thr Asp Ala Asn Asn
1640 1645 1650

Ile Glu Gly Gln Ala Ile Arg Tyr Gln Asn Arg Phe Leu Tyr Leu
1655 1660 1665

His Asp Asn Ile Tyr Tyr Phe Gly Asn Asn Ser Lys Ala Ala Thr
1670 1675 1680

Gly Trp Val Thr Ile Asp Gly Asn Arg Tyr Tyr Phe Glu Pro Asn
1685 1690 1695

Thr Ala Met Gly Ala Asn Gly Tyr Lys Thr Ile Asp Asn Lys Asn
1700 1705 1710

Phe Tyr Phe Arg Asn Gly Leu Pro Gln Ile Gly Val Phe Lys Gly
1715 1720 1725

Ser Asn Gly Phe Glu Tyr Phe Ala Pro Ala Asn Thr Asp Ala Asn
1730 1735 1740

Asn Ile Glu Gly Gln Ala Ile Arg Tyr Gln Asn Arg Phe Leu His
1745 1750 1755

Leu Leu Gly Lys Ile Tyr Tyr Phe Gly Asn Asn Ser Lys Ala Val
1760 1765 1770

Thr Gly Trp Gln Thr Ile Asn Gly Lys Val Tyr Tyr Phe Met Pro
1775 1780 1785

Asp Thr Ala Met Ala Ala Ala Gly Gly Leu Phe Glu Ile Asp Gly
1790 1795 1800

Val Ile Tyr Phe Phe Gly Val Asp Gly Val Lys Ala Pro Gly Ile
1805 1810 1815

Tyr Gly
1820

<210> 10
<211> 842
<212> PRT
<213> Clostridium difficile

<220>
<221> misc_feature
<222> (595)..(595)
<223> Xaa can be any naturally occurring amino acid

<400> 10

Met Glu Ile Val Asn Glu Asp Ile Leu Pro Asn Asn Gly Leu Met Gly
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Tyr Tyr Phe Thr Asp Glu His Phe Lys Asp Leu Lys Leu Met Ala Pro

20

25

30

Ile Lys Asp Gly Asn Leu Lys Phe Glu Glu Lys Lys Val Asp Lys Leu
 35 40 45

Leu Asp Lys Asp Lys Ser Asp Val Lys Ser Ile Arg Trp Thr Gly Arg
 50 55 60

Ile Ile Pro Ser Lys Asp Gly Glu Tyr Thr Leu Ser Thr Asp Arg Asp
 65 70 75 80

Asp Val Leu Met Gln Val Asn Thr Glu Ser Thr Ile Ser Asn Thr Leu
 85 90 95

Lys Val Asn Met Lys Lys Gly Lys Glu Tyr Lys Val Arg Ile Glu Leu
 100 105 110

Gln Asp Lys Asn Leu Gly Ser Ile Asp Asn Leu Ser Ser Pro Asn Leu
 115 120 125

Tyr Trp Glu Leu Asp Gly Met Lys Lys Ile Ile Pro Glu Glu Asn Leu
 130 135 140

Phe Leu Arg Asp Tyr Ser Asn Ile Glu Lys Asp Asp Pro Phe Ile Pro
 145 150 155 160

Asn Asn Asn Phe Phe Asp Pro Lys Leu Arg Ala Arg Arg Arg Lys Lys
 165 170 175

Arg Met Ser Asp Trp Glu Asp Glu Asp Leu Asp Thr Asp Asn Asp Asn
 180 185 190

Ile Pro Asp Ser Tyr Glu Arg Asn Gly Tyr Thr Ile Lys Asp Leu Ile
 195 200 205

Ala Val Lys Trp Glu Asp Ser Phe Ala Glu Gln Gly Tyr Lys Lys Tyr
 210 215 220

Val Ser Asn Tyr Leu Glu Ser Asn Thr Ala Gly Asp Pro Tyr Asp Tyr
 225 230 235 240

Glu Lys Ala Ser Gly Ser Phe Asp Lys Ala Ile Lys Thr Glu Ala Arg
245 250 255

Asp Pro Leu Val Ala Ala Tyr Pro Ile Val Gly Val Gly Met Glu Lys
260 265 270

Leu Ile Ile Ser Thr Asn Glu His Ala Ser Thr Asp Gln Gly Lys Thr
275 280 285

Val Ser Arg Ala Thr Thr Asn Ser Lys Thr Glu Ser Asn Thr Ala Gly
290 295 300

Val Ser Val Asn Val Gly Tyr Gln Asn Gly Phe Thr Ala Asn Val Thr
305 310 315 320

Thr Asn Tyr Ser His Thr Thr Asp Asn Ser Thr Ala Val Gln Asp Ser
325 330 335

Asn Gly Glu Ser Trp Asn Thr Gly Leu Ser Ile Asn Lys Gly Glu Ser
340 345 350

Ala Tyr Ile Asn Ala Asn Val Arg Tyr Tyr Asn Thr Gly Thr Ala Pro
355 360 365

Met Tyr Lys Val Thr Pro Thr Thr Asn Leu Val Leu Asp Gly Asp Thr
370 375 380

Leu Ser Thr Ile Lys Ala Gln Glu Asn Gln Ile Gly Asn Asn Leu Ser
385 390 395 400

Pro Gly Asp Thr Tyr Pro Lys Lys Gly Leu Ser Pro Leu Ala Leu Asn
405 410 415

Thr Met Asp Gln Phe Ser Ser Arg Leu Ile Pro Ile Asn Tyr Asp Gln
420 425 430

Leu Lys Lys Leu Asp Ala Gly Lys Gln Ile Lys Leu Glu Thr Thr Gln
435 440 445

Val Ser Gly Asn Phe Gly Thr Lys Asn Ser Ser Gly Gln Ile Val Thr

450

455

460

Glu Gly Asn Ser Trp Ser Asp Tyr Ile Ser Gln Ile Asp Ser Ile Ser
 465 470 475 480

Ala Ser Ile Ile Leu Asp Thr Glu Asn Glu Ser Tyr Glu Arg Arg Val
 485 490 495

Thr Ala Lys Asn Leu Gln Asp Pro Glu Asp Lys Thr Pro Glu Leu Thr
 500 505 510

Ile Gly Glu Ala Ile Glu Lys Ala Phe Gly Ala Thr Lys Lys Asp Gly
 515 520 525

Leu Leu Tyr Phe Asn Asp Ile Pro Ile Asp Glu Ser Cys Val Glu Leu
 530 535 540

Ile Phe Asp Asp Asn Thr Ala Asn Lys Ile Lys Asp Ser Leu Lys Thr
 545 550 555 560

Leu Ser Asp Lys Lys Ile Tyr Asn Val Lys Leu Glu Arg Gly Met Asn
 565 570 575

Ile Leu Ile Lys Thr Pro Thr Tyr Phe Thr Asn Phe Asp Asp Tyr Asn
 580 585 590

Asn Tyr Xaa Ser Thr Trp Ser Asn Val Asn Thr Thr Asn Gln Asp Gly
 595 600 605

Leu Gln Gly Ser Ala Asn Lys Leu Asn Gly Glu Thr Lys Ile Lys Ile
 610 615 620

Pro Met Ser Glu Leu Lys Pro Tyr Lys Arg Tyr Val Phe Ser Gly Tyr
 625 630 635 640

Ser Lys Asp Pro Leu Thr Ser Asn Ser Ile Ile Val Lys Ile Lys Ala
 645 650 655

Lys Glu Glu Lys Thr Asp Tyr Leu Val Pro Glu Gln Gly Tyr Thr Lys
 660 665 670

Phe Ser Tyr Glu Phe Glu Thr Thr Glu Lys Asp Ser Ser Asn Ile Glu
675 680 685

Ile Thr Leu Ile Gly Ser Gly Thr Thr Tyr Leu Asp Asn Leu Ser Ile
690 695 700

Thr Glu Leu Asn Ser Thr Pro Glu Ile Leu Asp Glu Pro Glu Val Lys
705 710 715 720

Ile Pro Thr Asp Gln Glu Ile Met Asp Ala His Lys Ile Tyr Phe Ala
725 730 735

Asp Leu Asn Phe Asn Pro Ser Thr Gly Asn Thr Tyr Ile Asn Gly Met
740 745 750

Tyr Phe Ala Pro Thr Gln Thr Asn Lys Glu Ala Leu Asp Tyr Ile Gln
755 760 765

Lys Tyr Arg Val Glu Ala Thr Leu Gln Tyr Ser Gly Phe Lys Asp Ile
770 775 780

Gly Thr Lys Asp Lys Glu Met Arg Asn Tyr Leu Gly Asp Pro Asn Gln
785 790 795 800

Pro Lys Thr Asn Tyr Val Asn Leu Arg Ser Tyr Phe Thr Gly Gly Glu
805 810 815

Asn Ile Met Thr Tyr Lys Lys Leu Arg Ile Tyr Ala Ile Thr Pro Asp
820 825 830

Asp Arg Glu Leu Leu Val Leu Ser Val Asp
835 840

<210> 11
<211> 536
<212> PRT
<213> Clostridium difficile

<400> 11

Met Val Ser Gly Leu Ile Tyr Ile Asn Asp Ser Leu Tyr Tyr Phe Lys
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Pro Pro Val Asn Asn Leu Ile Thr Gly Phe Val Thr Val Gly Asp Asp
20 25 30

Lys Tyr Tyr Phe Asn Pro Ile Asn Gly Gly Ala Ala Ser Ile Gly Glu
35 40 45

Thr Ile Ile Asp Asp Lys Asn Tyr Tyr Phe Asn Gln Ser Gly Val Leu
50 55 60

Gln Thr Gly Val Phe Ser Thr Glu Asp Gly Phe Lys Tyr Phe Ala Pro
65 70 75 80

Ala Asn Thr Leu Asp Glu Asn Leu Glu Gly Glu Ala Ile Asp Phe Thr
85 90 95

Gly Lys Leu Ile Ile Asp Glu Asn Ile Tyr Tyr Phe Asp Asp Asn Tyr
100 105 110

Arg Gly Ala Val Glu Trp Lys Glu Leu Asp Gly Glu Met His Tyr Phe
115 120 125

Ser Pro Glu Thr Gly Lys Ala Phe Lys Gly Leu Asn Gln Ile Gly Asp
130 135 140

Tyr Lys Tyr Tyr Phe Asn Ser Asp Gly Val Met Gln Lys Gly Phe Val
145 150 155 160

Ser Ile Asn Asp Asn Lys His Tyr Phe Asp Asp Ser Gly Val Met Lys
165 170 175

Val Gly Tyr Thr Glu Ile Asp Gly Lys His Phe Tyr Phe Ala Glu Asn
180 185 190

Gly Glu Met Gln Ile Gly Val Phe Asn Thr Glu Asp Gly Phe Lys Tyr
195 200 205

Phe Ala His His Asn Glu Asp Leu Gly Asn Glu Glu Gly Glu Glu Ile
210 215 220

Ser Tyr Ser Gly Ile Leu Asn Phe Asn Asn Lys Ile Tyr Tyr Phe Asp
225 230 235 240

Asp Ser Phe Thr Ala Val Val Gly Trp Lys Asp Leu Glu Asp Gly Ser
245 250 255

Lys Tyr Tyr Phe Asp Glu Asp Thr Ala Glu Ala Tyr Ile Gly Leu Ser
260 265 270

Leu Ile Asn Asp Gly Gln Tyr Tyr Phe Asn Asp Asp Gly Ile Met Gln
275 280 285

Val Gly Phe Val Thr Ile Asn Asp Lys Val Phe Tyr Phe Ser Asp Ser
290 295 300

Gly Ile Ile Glu Ser Gly Val Gln Asn Ile Asp Asp Asn Tyr Phe Tyr
305 310 315 320

Ile Asp Asp Asn Gly Ile Val Gln Ile Gly Val Phe Asp Thr Ser Asp
325 330 335

Gly Tyr Lys Tyr Phe Ala Pro Ala Asn Thr Val Asn Asp Asn Ile Tyr
340 345 350

Gly Gln Ala Val Glu Tyr Ser Gly Leu Val Arg Val Gly Glu Asp Val
355 360 365

Tyr Tyr Phe Gly Glu Thr Tyr Thr Ile Glu Thr Gly Trp Ile Tyr Asp
370 375 380

Met Glu Asn Glu Ser Asp Lys Tyr Tyr Phe Asn Pro Glu Thr Lys Lys
385 390 395 400

Ala Cys Lys Gly Ile Asn Leu Ile Asp Asp Ile Lys Tyr Tyr Phe Asp
405 410 415

Glu Lys Gly Ile Met Arg Thr Gly Leu Ile Ser Phe Glu Asn Asn Asn
420 425 430

Tyr Tyr Phe Asn Glu Asn Gly Glu Met Gln Phe Gly Tyr Ile Asn Ile
435 440 445

Glu Asp Lys Met Phe Tyr Phe Gly Glu Asp Gly Val Met Gln Ile Gly
450 455 460

Val Phe Asn Thr Pro Asp Gly Phe Lys Tyr Phe Ala His Gln Asn Thr
465 470 475 480

Leu Asp Glu Asn Phe Glu Gly Glu Ser Ile Asn Tyr Thr Gly Trp Leu
485 490 495

Asp Leu Asp Glu Lys Arg Tyr Tyr Phe Thr Asp Glu Tyr Ile Ala Ala
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Thr Gly Ser Val Ile Ile Asp Gly Glu Glu Tyr Tyr Phe Asp Pro Asp
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Thr Ala Gln Leu Val Ile Ser Glu
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<212> PRT
<213> Clostridium difficile

<400> 12

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Gln Asn Lys Phe Leu Thr Leu Asn Gly Lys Lys Tyr Tyr Phe Asp Asn
35 40 45

Asp Ser Lys Ala Val Thr Gly Trp Gln Thr Ile Asp Gly Lys Lys Tyr
50 55 60

Tyr Phe Asn Leu Asn Thr Ala Glu Ala Ala Thr Gly Trp Gln Thr Ile
65 70 75 80

Asp Gly Lys Lys Tyr Tyr Phe Asn Leu Asn Thr Ala Glu Ala Ala Thr

85

90

95

Gly Trp Gln Thr Ile Asp Gly Lys Lys Tyr Tyr Phe Asn Thr Asn Thr
 100 105 110

Phe Ile Ala Ser Thr Gly Tyr Thr Ser Ile Asn Gly Lys His Phe Tyr
 115 120 125

Phe Asn Thr Asp Gly Ile Met Gln Ile Gly Val Phe Lys Gly Pro Asn
 130 135 140

Gly Phe Glu Tyr Phe Ala Pro Ala Asn Thr Asp Ala Asn Asn Ile Glu
 145 150 155 160

Gly Gln Ala Ile Leu Tyr Gln Asn Lys Phe Leu Thr Leu Asn Gly Lys
 165 170 175

Lys Tyr Tyr Phe Gly Ser Asp Ser Lys Ala Val Thr Gly Leu Arg Thr
 180 185 190

Ile Asp Gly Lys Lys Tyr Tyr Phe Asn Thr Asn Thr Ala Val Ala Val
 195 200 205

Thr Gly Trp Gln Thr Ile Asn Gly Lys Lys Tyr Tyr Phe Asn Thr Asn
 210 215 220

Thr Ser Ile Ala Ser Thr Gly Tyr Thr Ile Ile Ser Gly Lys His Phe
 225 230 235 240

Tyr Phe Asn Thr Asp Gly Ile Met Gln Ile Gly Val Phe Lys Gly Pro
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Asp Gly Phe Glu Tyr Phe Ala Pro Ala Asn Thr Asp Ala Asn Asn Ile
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Glu Gly Gln Ala Ile Arg Tyr Gln Asn Arg Phe Leu Tyr Leu His Asp
 275 280 285

Asn Ile Tyr Tyr Phe Gly Asn Asn Ser Lys Ala Ala Thr Gly Trp Val
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Thr Ile Asp Gly Asn Arg Tyr Tyr Phe Glu Pro Asn Thr Ala Met Gly
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Ala Asn Gly Tyr Lys Thr Ile Asp Asn Lys Asn Phe Tyr Phe Arg Asn
325 330 335

Gly Leu Pro Gln Ile Gly Val Phe Lys Gly Ser Asn Gly Phe Glu Tyr
340 345 350

Phe Ala Pro Ala Asn Thr Asp Ala Asn Asn Ile Glu Gly Gln Ala Ile
355 360 365

Arg Tyr Gln Asn Arg Phe Leu His Leu Leu Gly Lys Ile Tyr Tyr Phe
370 375 380

Gly Asn Asn Ser Lys Ala Val Thr Gly Trp Gln Thr Ile Asn Gly Lys
385 390 395 400

Val Tyr Tyr Phe Met Pro Asp Thr Ala Met Ala Ala Ala Gly Gly Leu
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420 425 430

Ala Pro Gly Ile Tyr Gly
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<220>
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<222> (1787)..(1787)
<223> n is a, c, g, or t

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gaggaaaaga aggtcgataa gctgctcgac aaggataaga gcgacgttaa gtcaatcagg	180
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<210> 14
 <211> 2529
 <212> DNA
 <213> Clostridium difficile

<220>
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 <222> (1787)..(1787)
 <223> n is a, c, g, or t

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<210> 16
 <211> 1317
 <212> DNA
 <213> Clostridium difficile

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<210> 17
<211> 2307
<212> PRT
<213> Artificial Sequence

<220>
<223> Triple toxin vaccine BV1512

<220>
<221> misc_feature
<222> (588)..(588)
<223> Xaa can be any naturally occurring amino acid

<400> 17

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Ile Lys Asp Gly Asn Leu Lys Phe Glu Glu Lys Lys Val Asp Lys Leu
35 40 45

Leu Asp Lys Asp Lys Ser Asp Val Lys Ser Ile Arg Trp Thr Gly Arg
50 55 60

Ile Ile Pro Ser Lys Asp Gly Glu Tyr Thr Leu Ser Thr Asp Arg Asp
65 70 75 80

Asp Val Leu Met Gln Val Asn Thr Glu Ser Thr Ile Ser Asn Thr Leu
85 90 95

Lys Val Asn Met Lys Lys Gly Lys Glu Tyr Lys Val Arg Ile Glu Leu
100 105 110

Gln Asp Lys Asn Leu Gly Ser Ile Asp Asn Leu Ser Ser Pro Asn Leu
115 120 125

Tyr Trp Glu Leu Asp Gly Met Lys Lys Ile Ile Pro Glu Glu Asn Leu
130 135 140

Phe Leu Arg Asp Tyr Ser Asn Ile Glu Lys Asp Asp Pro Phe Ile Pro
145 150 155 160

Asn Asn Asn Phe Phe Asp Pro Lys Leu Met Ser Asp Trp Glu Asp Glu
165 170 175

Asp Leu Asp Thr Asp Asn Asp Asn Ile Pro Asp Ser Tyr Glu Arg Asn
180 185 190

Gly Tyr Thr Ile Lys Asp Leu Ile Ala Val Lys Trp Glu Asp Ser Phe
195 200 205

Ala Glu Gln Gly Tyr Lys Lys Tyr Val Ser Asn Tyr Leu Glu Ser Asn
210 215 220

Thr Ala Gly Asp Pro Tyr Thr Asp Tyr Glu Lys Ala Ser Gly Ser Phe
225 230 235 240

Asp Lys Ala Ile Lys Thr Glu Ala Arg Asp Pro Leu Val Ala Ala Tyr
245 250 255

Pro Ile Val Gly Val Gly Met Glu Lys Leu Ile Ile Ser Thr Asn Glu
260 265 270

His Ala Ser Thr Asp Gln Gly Lys Thr Val Ser Arg Ala Thr Thr Asn
275 280 285

Ser Lys Thr Glu Ser Asn Thr Ala Gly Val Ser Val Asn Val Gly Tyr
290 295 300

Gln Asn Gly Phe Thr Ala Asn Val Thr Thr Asn Tyr Ser His Thr Thr
305 310 315 320

Asp Asn Ser Thr Ala Val Gln Asp Ser Asn Gly Glu Ser Trp Asn Thr
325 330 335

Gly Leu Ser Ile Asn Lys Gly Glu Ser Ala Tyr Ile Asn Ala Asn Val
340 345 350

Arg Tyr Tyr Asn Thr Gly Thr Ala Pro Met Tyr Lys Val Thr Pro Thr
355 360 365

Thr Asn Leu Val Leu Asp Gly Asp Thr Leu Ser Thr Ile Lys Ala Gln
370 375 380

Glu Asn Gln Ile Gly Asn Asn Leu Ser Pro Gly Asp Thr Tyr Pro Lys
385 390 395 400

Lys Gly Leu Ser Pro Leu Ala Leu Asn Thr Met Asp Gln Phe Ser Ser
405 410 415

Arg Leu Ile Pro Ile Asn Tyr Asp Gln Leu Lys Lys Leu Asp Ala Gly
420 425 430

Lys Gln Ile Lys Leu Glu Thr Thr Gln Val Ser Gly Asn Phe Gly Thr
435 440 445

Lys Asn Ser Ser Gly Gln Ile Val Thr Glu Gly Asn Ser Trp Ser Asp
450 455 460

Tyr Ile Ser Gln Ile Asp Ser Ile Ser Ala Ser Ile Ile Leu Asp Thr
465 470 475 480

Glu Asn Glu Ser Tyr Glu Arg Arg Val Thr Ala Lys Asn Leu Gln Asp
485 490 495

Pro Glu Asp Lys Thr Pro Glu Leu Thr Ile Gly Glu Ala Ile Glu Lys
500 505 510

Ala Phe Gly Ala Thr Lys Lys Asp Gly Leu Leu Tyr Phe Asn Asp Ile
515 520 525

Pro Ile Asp Glu Ser Cys Val Glu Leu Ile Phe Asp Asp Asn Thr Ala
530 535 540

Asn Lys Ile Lys Asp Ser Leu Lys Thr Leu Ser Asp Lys Lys Ile Tyr
545 550 555 560

Asn Val Lys Leu Glu Arg Gly Met Asn Ile Leu Ile Lys Thr Pro Thr
565 570 575

Tyr Phe Thr Asn Phe Asp Asp Tyr Asn Asn Tyr Xaa Ser Thr Trp Ser
580 585 590

Asn Val Asn Thr Thr Asn Gln Asp Gly Leu Gln Gly Ser Ala Asn Lys
595 600 605

Leu Asn Gly Glu Thr Lys Ile Lys Ile Pro Met Ser Glu Leu Lys Pro
610 615 620

Tyr Lys Arg Tyr Val Phe Ser Gly Tyr Ser Lys Asp Pro Leu Thr Ser
625 630 635 640

Asn Ser Ile Ile Val Lys Ile Lys Ala Lys Glu Glu Lys Thr Asp Tyr
645 650 655

Leu Val Pro Glu Gln Gly Tyr Thr Lys Phe Ser Tyr Glu Phe Glu Thr
660 665 670

Thr Glu Lys Asp Ser Ser Asn Ile Glu Ile Thr Leu Ile Gly Ser Gly
675 680 685

Thr Thr Tyr Leu Asp Asn Leu Ser Ile Thr Glu Leu Asn Ser Thr Pro
690 695 700

Glu Ile Leu Asp Glu Pro Glu Val Lys Ile Pro Thr Asp Gln Glu Ile
705 710 715 720

Met Asp Ala His Lys Ile Tyr Phe Ala Asp Leu Asn Phe Asn Pro Ser
725 730 735

Thr Gly Asn Thr Tyr Ile Asn Gly Met Tyr Phe Ala Pro Thr Gln Thr
740 745 750

Asn Lys Glu Ala Leu Asp Tyr Ile Gln Lys Tyr Arg Val Glu Ala Thr
755 760 765

Leu Gln Tyr Ser Gly Phe Lys Asp Ile Gly Thr Lys Asp Lys Glu Met
770 775 780

Arg Asn Tyr Leu Gly Asp Pro Asn Gln Pro Lys Thr Asn Tyr Val Asn
785 790 795 800

Leu Arg Ser Tyr Phe Thr Gly Gly Glu Asn Ile Met Thr Tyr Lys Lys
805 810 815

Leu Arg Ile Tyr Ala Ile Thr Pro Asp Asp Arg Glu Leu Leu Val Leu
820 825 830

Ser Val Asp Ala Ser Met Gln Glu Ile Arg Asn Asn Ser Asn Ser Ser
835 840 845

Asp Ile Glu Leu Glu Glu Lys Val Met Leu Thr Glu Cys Glu Ile Asn
850 855 860

Val Ile Ser Asn Ile Asp Thr Gln Ile Val Glu Glu Arg Ile Glu Glu
865 870 875 880

Ala Lys Asn Leu Thr Ser Asp Ser Ile Asn Tyr Ile Lys Asp Glu Phe
885 890 895

Lys Leu Ile Glu Ser Ile Ser Asp Ala Leu Cys Asp Leu Lys Gln Gln
900 905 910

Asn Glu Leu Glu Asp Ser His Phe Ile Ser Phe Glu Asp Ile Ser Glu
915 920 925

Thr Asp Glu Gly Phe Ser Ile Arg Phe Ile Asn Lys Glu Thr Gly Glu
930 935 940

Ser Ile Phe Val Glu Thr Glu Lys Thr Ile Phe Ser Glu Tyr Ala Asn
945 950 955 960

His Ile Thr Glu Glu Ile Ser Lys Ile Lys Gly Thr Ile Phe Asp Thr
965 970 975

Val Asn Gly Lys Leu Val Lys Lys Val Asn Leu Asp Thr Thr His Glu
980 985 990

Val Asn Thr Leu Asn Ala Ala Phe Phe Ile Gln Ser Leu Ile Glu Tyr
995 1000 1005

Asn Ser Ser Lys Glu Ser Leu Ser Asn Leu Ser Val Ala Met Lys
1010 1015 1020

Val Gln Val Tyr Ala Gln Leu Phe Ser Thr Gly Leu Asn Thr Ile
1025 1030 1035

Thr Asp Ala Ala Lys Val Val Glu Leu Val Ser Thr Ala Leu Asp
1040 1045 1050

Glu Thr Ile Asp Leu Leu Pro Thr Leu Ser Glu Gly Leu Pro Ile
1055 1060 1065

Ile Ala Thr Ile Ile Asp Gly Val Ser Leu Gly Ala Ala Ile Lys
1070 1075 1080

Glu Leu Ser Glu Thr Ser Asp Pro Leu Leu Arg Gln Glu Ile Glu
1085 1090 1095

Ala Lys Ile Gly Ile Met Ala Val Asn Leu Thr Thr Ala Thr Thr
1100 1105 1110

Ala Ile Ile Thr Ser Ser Leu Gly Ile Ala Ser Gly Phe Ser Ile
1115 1120 1125

Leu Leu Val Pro Leu Ala Gly Ile Ser Ala Gly Ile Pro Ser Leu
1130 1135 1140

Val Asn Asn Glu Leu Val Leu Arg Asp Lys Ala Thr Lys Val Val
1145 1150 1155

Asp	Tyr	Phe	Lys	His	Val	Ser	Leu	Val	Glu	Thr	Glu	Gly	Val	Phe
1160						1165					1170			
Thr	Leu	Leu	Asp	Asp	Lys	Ile	Met	Met	Pro	Gln	Asp	Asp	Leu	Val
1175						1180					1185			
Ile	Ser	Glu	Ile	Asp	Phe	Asn	Asn	Asn	Ser	Ile	Val	Leu	Gly	Lys
1190						1195					1200			
Cys	Glu	Ile	Trp	Arg	Met	Glu	Gly	Gly	Ser	Gly	His	Thr	Val	Thr
1205						1210					1215			
Asp	Asp	Ile	Asp	His	Phe	Phe	Ser	Ala	Pro	Ser	Ile	Thr	Tyr	Arg
1220						1225					1230			
Glu	Pro	His	Leu	Ser	Ile	Tyr	Asp	Val	Leu	Glu	Val	Gln	Lys	Glu
1235						1240					1245			
Glu	Leu	Asp	Leu	Ser	Lys	Asp	Leu	Met	Val	Leu	Pro	Asn	Ala	Pro
1250						1255					1260			
Asn	Arg	Val	Phe	Ala	Trp	Glu	Thr	Gly	Trp	Thr	Pro	Gly	Leu	Arg
1265						1270					1275			
Ser	Leu	Glu	Asn	Asp	Gly	Thr	Lys	Leu	Leu	Asp	Arg	Ile	Arg	Asp
1280						1285					1290			
Asn	Tyr	Glu	Gly	Glu	Phe	Tyr	Trp	Arg	Tyr	Phe	Ala	Phe	Ile	Ala
1295						1300					1305			
Asp	Ala	Leu	Ile	Thr	Thr	Leu	Lys	Pro	Arg	Tyr	Glu	Asp	Thr	Asn
1310						1315					1320			
Ile	Arg	Ile	Asn	Leu	Asp	Ser	Asn	Thr	Arg	Ser	Phe	Ile	Val	Pro
1325						1330					1335			
Ile	Ile	Thr	Thr	Glu	Tyr	Ile	Arg	Glu	Lys	Leu	Ser	Tyr	Ser	Phe
1340						1345					1350			
Tyr	Gly	Ser	Gly	Gly	Thr	Tyr	Ala	Leu	Ser	Leu	Ser	Gln	Tyr	Asn
1355						1360					1365			

Met Gly Ile Asn Ile Glu Leu Ser Glu Ser Asp Val Trp Ile Ile
1370 1375 1380

Asp Val Asp Asn Val Val Arg Asp Val Thr Ile Glu Ser Asp Lys
1385 1390 1395

Ile Lys Lys Gly Asp Leu Ile Glu Gly Ile Leu Ser Thr Leu Ser
1400 1405 1410

Ile Glu Glu Asn Lys Ile Ile Leu Asn Ser His Glu Ile Asn Phe
1415 1420 1425

Ser Gly Glu Val Asn Gly Ser Asn Gly Phe Val Ser Leu Thr Phe
1430 1435 1440

Ser Ile Leu Glu Gly Ile Asn Ala Ile Ile Glu Val Asp Leu Leu
1445 1450 1455

Ser Lys Ser Tyr Lys Leu Leu Ile Ser Gly Glu Leu Lys Ile Leu
1460 1465 1470

Met Leu Asn Ser Asn His Ile Gln Gln Lys Ile Asp Tyr Ile Gly
1475 1480 1485

Phe Asn Ser Glu Leu Gln Lys Asn Ile Pro Tyr Ser Phe Val Asp
1490 1495 1500

Ser Glu Gly Lys Glu Asn Gly Phe Ile Asn Gly Ser Thr Lys Glu
1505 1510 1515

Gly Leu Phe Val Ser Glu Leu Pro Asp Val Val Leu Ile Ser Lys
1520 1525 1530

Val Tyr Met Asp Asp Ser Lys Pro Ser Phe Gly Tyr Tyr Ser Asn
1535 1540 1545

Asn Leu Lys Asp Val Lys Val Ile Thr Lys Asp Asn Val Asn Ile
1550 1555 1560

Leu Thr Gly Tyr Tyr Leu Lys Asp Asp Ile Lys Ile Ser Leu Ser
1565 1570 1575

Leu Thr Leu Gln Asp Glu Lys Thr Ile Lys Leu Asn Ser Val His
1580 1585 1590

Leu Asp Glu Ser Gly Val Ala Glu Ile Leu Lys Phe Met Asn Arg
1595 1600 1605

Lys Gly Asn Thr Asn Thr Ser Asp Ser Leu Met Ser Phe Leu Glu
1610 1615 1620

Ser Met Asn Ile Lys Ser Ile Phe Val Asn Phe Leu Gln Ser Asn
1625 1630 1635

Ile Lys Phe Ile Leu Asp Ala Asn Phe Ile Ile Ser Gly Thr Thr
1640 1645 1650

Ser Ile Gly Gln Phe Glu Phe Ile Cys Asp Glu Asn Asp Asn Ile
1655 1660 1665

Gln Pro Tyr Phe Ile Lys Phe Asn Thr Leu Glu Thr Asn Tyr Thr
1670 1675 1680

Leu Tyr Val Gly Asn Arg Gln Asn Met Ile Val Glu Pro Asn Tyr
1685 1690 1695

Asp Leu Asp Asp Ser Gly Asp Ile Ser Ser Thr Val Ile Asn Phe
1700 1705 1710

Ser Gln Lys Tyr Leu Tyr Gly Ile Asp Ser Cys Val Asn Lys Val
1715 1720 1725

Val Ile Ser Pro Asn Ile Tyr Thr Asp Glu Ile Asn Ile Thr Pro
1730 1735 1740

Val Tyr Glu Thr Asn Asn Thr Tyr Pro Glu Val Ile Val Leu Asp
1745 1750 1755

Ala Asn Tyr Ile Asn Glu Lys Ile Asn Val Asn Ile Asn Asp Leu
1760 1765 1770

Ser Ile Arg Tyr Val Trp Ser Asn Asp Gly Asn Asp Phe Ile Leu
1775 1780 1785

Met Ser Thr Ser Glu Glu Asn Lys Val Ser Gln Val Lys Ile Arg
1790 1795 1800

Phe Val Asn Val Phe Lys Asp Lys Thr Leu Ala Asn Lys Leu Ser
1805 1810 1815

Phe Asn Phe Ser Asp Lys Gln Asp Val Pro Val Ser Glu Ile Ile
1820 1825 1830

Leu Ser Phe Thr Pro Ser Tyr Tyr Glu Asp Gly Leu Ile Gly Tyr
1835 1840 1845

Asp Leu Gly Leu Val Ser Leu Tyr Asn Glu Lys Phe Tyr Ile Asn
1850 1855 1860

Asn Phe Gly Met Ser Arg Met Val Thr Gly Val Phe Lys Gly Pro
1865 1870 1875

Asn Gly Phe Glu Tyr Phe Ala Pro Ala Asn Thr His Asn Asn Asn
1880 1885 1890

Ile Glu Gly Gln Ala Ile Val Tyr Gln Asn Lys Phe Leu Thr Leu
1895 1900 1905

Asn Gly Lys Lys Tyr Tyr Phe Asp Asn Asp Ser Lys Ala Val Thr
1910 1915 1920

Gly Trp Gln Thr Ile Asp Gly Lys Lys Tyr Tyr Phe Asn Leu Asn
1925 1930 1935

Thr Ala Glu Ala Ala Thr Gly Trp Gln Thr Ile Asp Gly Lys Lys
1940 1945 1950

Tyr Tyr Phe Asn Leu Asn Thr Ala Glu Ala Ala Thr Gly Trp Gln
1955 1960 1965

Thr 1970	Ile	Asp	Gly	Lys	Lys	Tyr 1975	Tyr	Phe	Asn	Thr	Asn 1980	Thr	Phe	Ile
Ala 1985	Ser	Thr	Gly	Tyr	Thr	Ser 1990	Ile	Asn	Gly	Lys	His 1995	Phe	Tyr	Phe
Asn 2000	Thr	Asp	Gly	Ile	Met	Gln 2005	Ile	Gly	Val	Phe	Lys 2010	Gly	Pro	Asn
Gly 2015	Phe	Glu	Tyr	Phe	Ala	Pro 2020	Ala	Asn	Thr	Asp	Ala 2025	Asn	Asn	Ile
Glu 2030	Gly	Gln	Ala	Ile	Leu	Tyr 2035	Gln	Asn	Lys	Phe	Leu 2040	Thr	Leu	Asn
Gly 2045	Lys	Lys	Tyr	Tyr	Phe	Gly 2050	Ser	Asp	Ser	Lys	Ala 2055	Val	Thr	Gly
Leu 2060	Arg	Thr	Ile	Asp	Gly	Lys 2065	Lys	Tyr	Tyr	Phe	Asn 2070	Thr	Asn	Thr
Ala 2075	Val	Ala	Val	Thr	Gly	Trp 2080	Gln	Thr	Ile	Asn	Gly 2085	Lys	Lys	Tyr
Tyr 2090	Phe	Asn	Thr	Asn	Thr	Ser 2095	Ile	Ala	Ser	Thr	Gly 2100	Tyr	Thr	Ile
Ile 2105	Ser	Gly	Lys	His	Phe	Tyr 2110	Phe	Asn	Thr	Asp	Gly 2115	Ile	Met	Gln
Ile 2120	Gly	Val	Phe	Lys	Gly	Pro 2125	Asp	Gly	Phe	Glu	Tyr 2130	Phe	Ala	Pro
Ala 2135	Asn	Thr	Asp	Ala	Asn	Asn 2140	Ile	Glu	Gly	Gln	Ala 2145	Ile	Arg	Tyr
Gln 2150	Asn	Arg	Phe	Leu	Tyr	Leu 2155	His	Asp	Asn	Ile	Tyr 2160	Tyr	Phe	Gly
Asn 2165	Asn	Ser	Lys	Ala	Ala	Thr 2170	Gly	Trp	Val	Thr	Ile 2175	Asp	Gly	Asn

Arg Tyr Tyr Phe Glu Pro Asn Thr Ala Met Gly Ala Asn Gly Tyr
2180 2185 2190

Lys Thr Ile Asp Asn Lys Asn Phe Tyr Phe Arg Asn Gly Leu Pro
2195 2200 2205

Gln Ile Gly Val Phe Lys Gly Ser Asn Gly Phe Glu Tyr Phe Ala
2210 2215 2220

Pro Ala Asn Thr Asp Ala Asn Asn Ile Glu Gly Gln Ala Ile Arg
2225 2230 2235

Tyr Gln Asn Arg Phe Leu His Leu Leu Gly Lys Ile Tyr Tyr Phe
2240 2245 2250

Gly Asn Asn Ser Lys Ala Val Thr Gly Trp Gln Thr Ile Asn Gly
2255 2260 2265

Lys Val Tyr Tyr Phe Met Pro Asp Thr Ala Met Ala Ala Ala Gly
2270 2275 2280

Gly Leu Phe Glu Ile Asp Gly Val Ile Tyr Phe Phe Gly Val Asp
2285 2290 2295

Gly Val Lys Ala Pro Gly Ile Tyr Gly
2300 2305

<210> 18
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<212> PRT
<213> Clostridium difficile

<220>
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<223> Xaa can be any naturally occurring amino acid

<400> 18

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Tyr Tyr Phe Thr Asp Glu His Phe Lys Asp Leu Lys Leu Met Ala Pro
20 25 30

Ile Lys Asp Gly Asn Leu Lys Phe Glu Glu Lys Lys Val Asp Lys Leu
35 40 45

Leu Asp Lys Asp Lys Ser Asp Val Lys Ser Ile Arg Trp Thr Gly Arg
50 55 60

Ile Ile Pro Ser Lys Asp Gly Glu Tyr Thr Leu Ser Thr Asp Arg Asp
65 70 75 80

Asp Val Leu Met Gln Val Asn Thr Glu Ser Thr Ile Ser Asn Thr Leu
85 90 95

Lys Val Asn Met Lys Lys Gly Lys Glu Tyr Lys Val Arg Ile Glu Leu
100 105 110

Gln Asp Lys Asn Leu Gly Ser Ile Asp Asn Leu Ser Ser Pro Asn Leu
115 120 125

Tyr Trp Glu Leu Asp Gly Met Lys Lys Ile Ile Pro Glu Glu Asn Leu
130 135 140

Phe Leu Arg Asp Tyr Ser Asn Ile Glu Lys Asp Asp Pro Phe Ile Pro
145 150 155 160

Asn Asn Asn Phe Phe Asp Pro Lys Leu Met Ser Asp Trp Glu Asp Glu
165 170 175

Asp Leu Asp Thr Asp Asn Asp Asn Ile Pro Asp Ser Tyr Glu Arg Asn
180 185 190

Gly Tyr Thr Ile Lys Asp Leu Ile Ala Val Lys Trp Glu Asp Ser Phe
195 200 205

Ala Glu Gln Gly Tyr Lys Lys Tyr Val Ser Asn Tyr Leu Glu Ser Asn
210 215 220

Thr Ala Gly Asp Pro Tyr Thr Asp Tyr Glu Lys Ala Ser Gly Ser Phe

225		230		235		240									
Asp	Lys	Ala	Ile	Lys	Thr	Glu	Ala	Arg	Asp	Pro	Leu	Val	Ala	Ala	Tyr
			245						250					255	
Pro	Ile	Val	Gly	Val	Gly	Met	Glu	Lys	Leu	Ile	Ile	Ser	Thr	Asn	Glu
			260					265					270		
His	Ala	Ser	Thr	Asp	Gln	Gly	Lys	Thr	Val	Ser	Arg	Ala	Thr	Thr	Asn
		275					280					285			
Ser	Lys	Thr	Glu	Ser	Asn	Thr	Ala	Gly	Val	Ser	Val	Asn	Val	Gly	Tyr
	290					295					300				
Gln	Asn	Gly	Phe	Thr	Ala	Asn	Val	Thr	Thr	Asn	Tyr	Ser	His	Thr	Thr
305					310					315					320
Asp	Asn	Ser	Thr	Ala	Val	Gln	Asp	Ser	Asn	Gly	Glu	Ser	Trp	Asn	Thr
				325					330					335	
Gly	Leu	Ser	Ile	Asn	Lys	Gly	Glu	Ser	Ala	Tyr	Ile	Asn	Ala	Asn	Val
			340					345					350		
Arg	Tyr	Tyr	Asn	Thr	Gly	Thr	Ala	Pro	Met	Tyr	Lys	Val	Thr	Pro	Thr
		355					360					365			
Thr	Asn	Leu	Val	Leu	Asp	Gly	Asp	Thr	Leu	Ser	Thr	Ile	Lys	Ala	Gln
	370					375					380				
Glu	Asn	Gln	Ile	Gly	Asn	Asn	Leu	Ser	Pro	Gly	Asp	Thr	Tyr	Pro	Lys
385					390					395					400
Lys	Gly	Leu	Ser	Pro	Leu	Ala	Leu	Asn	Thr	Met	Asp	Gln	Phe	Ser	Ser
				405					410					415	
Arg	Leu	Ile	Pro	Ile	Asn	Tyr	Asp	Gln	Leu	Lys	Lys	Leu	Asp	Ala	Gly
			420					425					430		
Lys	Gln	Ile	Lys	Leu	Glu	Thr	Thr	Gln	Val	Ser	Gly	Asn	Phe	Gly	Thr
		435					440					445			

Lys Asn Ser Ser Gly Gln Ile Val Thr Glu Gly Asn Ser Trp Ser Asp
450 455 460

Tyr Ile Ser Gln Ile Asp Ser Ile Ser Ala Ser Ile Ile Leu Asp Thr
465 470 475 480

Glu Asn Glu Ser Tyr Glu Arg Arg Val Thr Ala Lys Asn Leu Gln Asp
485 490 495

Pro Glu Asp Lys Thr Pro Glu Leu Thr Ile Gly Glu Ala Ile Glu Lys
500 505 510

Ala Phe Gly Ala Thr Lys Lys Asp Gly Leu Leu Tyr Phe Asn Asp Ile
515 520 525

Pro Ile Asp Glu Ser Cys Val Glu Leu Ile Phe Asp Asp Asn Thr Ala
530 535 540

Asn Lys Ile Lys Asp Ser Leu Lys Thr Leu Ser Asp Lys Lys Ile Tyr
545 550 555 560

Asn Val Lys Leu Glu Arg Gly Met Asn Ile Leu Ile Lys Thr Pro Thr
565 570 575

Tyr Phe Thr Asn Phe Asp Asp Tyr Asn Asn Tyr Xaa Ser Thr Trp Ser
580 585 590

Asn Val Asn Thr Thr Asn Gln Asp Gly Leu Gln Gly Ser Ala Asn Lys
595 600 605

Leu Asn Gly Glu Thr Lys Ile Lys Ile Pro Met Ser Glu Leu Lys Pro
610 615 620

Tyr Lys Arg Tyr Val Phe Ser Gly Tyr Ser Lys Asp Pro Leu Thr Ser
625 630 635 640

Asn Ser Ile Ile Val Lys Ile Lys Ala Lys Glu Glu Lys Thr Asp Tyr
645 650 655

Leu Val Pro Glu Gln Gly Tyr Thr Lys Phe Ser Tyr Glu Phe Glu Thr

660

665

670

Thr Glu Lys Asp Ser Ser Asn Ile Glu Ile Thr Leu Ile Gly Ser Gly
 675 680 685

Thr Thr Tyr Leu Asp Asn Leu Ser Ile Thr Glu Leu Asn Ser Thr Pro
 690 695 700

Glu Ile Leu Asp Glu Pro Glu Val Lys Ile Pro Thr Asp Gln Glu Ile
 705 710 715 720

Met Asp Ala His Lys Ile Tyr Phe Ala Asp Leu Asn Phe Asn Pro Ser
 725 730 735

Thr Gly Asn Thr Tyr Ile Asn Gly Met Tyr Phe Ala Pro Thr Gln Thr
 740 745 750

Asn Lys Glu Ala Leu Asp Tyr Ile Gln Lys Tyr Arg Val Glu Ala Thr
 755 760 765

Leu Gln Tyr Ser Gly Phe Lys Asp Ile Gly Thr Lys Asp Lys Glu Met
 770 775 780

Arg Asn Tyr Leu Gly Asp Pro Asn Gln Pro Lys Thr Asn Tyr Val Asn
 785 790 795 800

Leu Arg Ser Tyr Phe Thr Gly Gly Glu Asn Ile Met Thr Tyr Lys Lys
 805 810 815

Leu Arg Ile Tyr Ala Ile Thr Pro Asp Asp Arg Glu Leu Leu Val Leu
 820 825 830

Ser Val Asp
 835

<210> 19

<211> 1030

<212> PRT

<213> Clostridium difficile

<400> 19

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Glu Lys Val Met Leu Thr Glu Cys Glu Ile Asn Val Ile Ser Asn Ile
20 25 30

Asp Thr Gln Ile Val Glu Glu Arg Ile Glu Glu Ala Lys Asn Leu Thr
35 40 45

Ser Asp Ser Ile Asn Tyr Ile Lys Asp Glu Phe Lys Leu Ile Glu Ser
50 55 60

Ile Ser Asp Ala Leu Cys Asp Leu Lys Gln Gln Asn Glu Leu Glu Asp
65 70 75 80

Ser His Phe Ile Ser Phe Glu Asp Ile Ser Glu Thr Asp Glu Gly Phe
85 90 95

Ser Ile Arg Phe Ile Asn Lys Glu Thr Gly Glu Ser Ile Phe Val Glu
100 105 110

Thr Glu Lys Thr Ile Phe Ser Glu Tyr Ala Asn His Ile Thr Glu Glu
115 120 125

Ile Ser Lys Ile Lys Gly Thr Ile Phe Asp Thr Val Asn Gly Lys Leu
130 135 140

Val Lys Lys Val Asn Leu Asp Thr Thr His Glu Val Asn Thr Leu Asn
145 150 155 160

Ala Ala Phe Phe Ile Gln Ser Leu Ile Glu Tyr Asn Ser Ser Lys Glu
165 170 175

Ser Leu Ser Asn Leu Ser Val Ala Met Lys Val Gln Val Tyr Ala Gln
180 185 190

Leu Phe Ser Thr Gly Leu Asn Thr Ile Thr Asp Ala Ala Lys Val Val
195 200 205

Glu Leu Val Ser Thr Ala Leu Asp Glu Thr Ile Asp Leu Leu Pro Thr
210 215 220

Leu Ser Glu Gly Leu Pro Ile Ile Ala Thr Ile Ile Asp Gly Val Ser
225 230 235 240

Leu Gly Ala Ala Ile Lys Glu Leu Ser Glu Thr Ser Asp Pro Leu Leu
245 250 255

Arg Gln Glu Ile Glu Ala Lys Ile Gly Ile Met Ala Val Asn Leu Thr
260 265 270

Thr Ala Thr Thr Ala Ile Ile Thr Ser Ser Leu Gly Ile Ala Ser Gly
275 280 285

Phe Ser Ile Leu Leu Val Pro Leu Ala Gly Ile Ser Ala Gly Ile Pro
290 295 300

Ser Leu Val Asn Asn Glu Leu Val Leu Arg Asp Lys Ala Thr Lys Val
305 310 315 320

Val Asp Tyr Phe Lys His Val Ser Leu Val Glu Thr Glu Gly Val Phe
325 330 335

Thr Leu Leu Asp Asp Lys Ile Met Met Pro Gln Asp Asp Leu Val Ile
340 345 350

Ser Glu Ile Asp Phe Asn Asn Asn Ser Ile Val Leu Gly Lys Cys Glu
355 360 365

Ile Trp Arg Met Glu Gly Gly Ser Gly His Thr Val Thr Asp Asp Ile
370 375 380

Asp His Phe Phe Ser Ala Pro Ser Ile Thr Tyr Arg Glu Pro His Leu
385 390 395 400

Ser Ile Tyr Asp Val Leu Glu Val Gln Lys Glu Glu Leu Asp Leu Ser
405 410 415

Lys Asp Leu Met Val Leu Pro Asn Ala Pro Asn Arg Val Phe Ala Trp
420 425 430

Glu Thr Gly Trp Thr Pro Gly Leu Arg Ser Leu Glu Asn Asp Gly Thr
435 440 445

Lys Leu Leu Asp Arg Ile Arg Asp Asn Tyr Glu Gly Glu Phe Tyr Trp
450 455 460

Arg Tyr Phe Ala Phe Ile Ala Asp Ala Leu Ile Thr Thr Leu Lys Pro
465 470 475 480

Arg Tyr Glu Asp Thr Asn Ile Arg Ile Asn Leu Asp Ser Asn Thr Arg
485 490 495

Ser Phe Ile Val Pro Ile Ile Thr Thr Glu Tyr Ile Arg Glu Lys Leu
500 505 510

Ser Tyr Ser Phe Tyr Gly Ser Gly Gly Thr Tyr Ala Leu Ser Leu Ser
515 520 525

Gln Tyr Asn Met Gly Ile Asn Ile Glu Leu Ser Glu Ser Asp Val Trp
530 535 540

Ile Ile Asp Val Asp Asn Val Val Arg Asp Val Thr Ile Glu Ser Asp
545 550 555 560

Lys Ile Lys Lys Gly Asp Leu Ile Glu Gly Ile Leu Ser Thr Leu Ser
565 570 575

Ile Glu Glu Asn Lys Ile Ile Leu Asn Ser His Glu Ile Asn Phe Ser
580 585 590

Gly Glu Val Asn Gly Ser Asn Gly Phe Val Ser Leu Thr Phe Ser Ile
595 600 605

Leu Glu Gly Ile Asn Ala Ile Ile Glu Val Asp Leu Leu Ser Lys Ser
610 615 620

Tyr Lys Leu Leu Ile Ser Gly Glu Leu Lys Ile Leu Met Leu Asn Ser
625 630 635 640

Asn His Ile Gln Gln Lys Ile Asp Tyr Ile Gly Phe Asn Ser Glu Leu
645 650 655

Gln Lys Asn Ile Pro Tyr Ser Phe Val Asp Ser Glu Gly Lys Glu Asn
660 665 670

Gly Phe Ile Asn Gly Ser Thr Lys Glu Gly Leu Phe Val Ser Glu Leu
675 680 685

Pro Asp Val Val Leu Ile Ser Lys Val Tyr Met Asp Asp Ser Lys Pro
690 695 700

Ser Phe Gly Tyr Tyr Ser Asn Asn Leu Lys Asp Val Lys Val Ile Thr
705 710 715 720

Lys Asp Asn Val Asn Ile Leu Thr Gly Tyr Tyr Leu Lys Asp Asp Ile
725 730 735

Lys Ile Ser Leu Ser Leu Thr Leu Gln Asp Glu Lys Thr Ile Lys Leu
740 745 750

Asn Ser Val His Leu Asp Glu Ser Gly Val Ala Glu Ile Leu Lys Phe
755 760 765

Met Asn Arg Lys Gly Asn Thr Asn Thr Ser Asp Ser Leu Met Ser Phe
770 775 780

Leu Glu Ser Met Asn Ile Lys Ser Ile Phe Val Asn Phe Leu Gln Ser
785 790 795 800

Asn Ile Lys Phe Ile Leu Asp Ala Asn Phe Ile Ile Ser Gly Thr Thr
805 810 815

Ser Ile Gly Gln Phe Glu Phe Ile Cys Asp Glu Asn Asp Asn Ile Gln
820 825 830

Pro Tyr Phe Ile Lys Phe Asn Thr Leu Glu Thr Asn Tyr Thr Leu Tyr
835 840 845

Val Gly Asn Arg Gln Asn Met Ile Val Glu Pro Asn Tyr Asp Leu Asp
850 855 860

Asp Ser Gly Asp Ile Ser Ser Thr Val Ile Asn Phe Ser Gln Lys Tyr
865 870 875 880

Leu Tyr Gly Ile Asp Ser Cys Val Asn Lys Val Val Ile Ser Pro Asn
885 890 895

Ile Tyr Thr Asp Glu Ile Asn Ile Thr Pro Val Tyr Glu Thr Asn Asn
900 905 910

Thr Tyr Pro Glu Val Ile Val Leu Asp Ala Asn Tyr Ile Asn Glu Lys
915 920 925

Ile Asn Val Asn Ile Asn Asp Leu Ser Ile Arg Tyr Val Trp Ser Asn
930 935 940

Asp Gly Asn Asp Phe Ile Leu Met Ser Thr Ser Glu Glu Asn Lys Val
945 950 955 960

Ser Gln Val Lys Ile Arg Phe Val Asn Val Phe Lys Asp Lys Thr Leu
965 970 975

Ala Asn Lys Leu Ser Phe Asn Phe Ser Asp Lys Gln Asp Val Pro Val
980 985 990

Ser Glu Ile Ile Leu Ser Phe Thr Pro Ser Tyr Tyr Glu Asp Gly Leu
995 1000 1005

Ile Gly Tyr Asp Leu Gly Leu Val Ser Leu Tyr Asn Glu Lys Phe
1010 1015 1020

Tyr Ile Asn Asn Phe Gly Met
1025 1030

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<211> 438
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<213> Clostridium difficile

<400> 20

Met Val Thr Gly Val Phe Lys Gly Pro Asn Gly Phe Glu Tyr Phe Ala
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Pro Ala Asn Thr His Asn Asn Asn Ile Glu Gly Gln Ala Ile Val Tyr
20 25 30

Gln Asn Lys Phe Leu Thr Leu Asn Gly Lys Lys Tyr Tyr Phe Asp Asn
35 40 45

Asp Ser Lys Ala Val Thr Gly Trp Gln Thr Ile Asp Gly Lys Lys Tyr
50 55 60

Tyr Phe Asn Leu Asn Thr Ala Glu Ala Ala Thr Gly Trp Gln Thr Ile
65 70 75 80

Asp Gly Lys Lys Tyr Tyr Phe Asn Leu Asn Thr Ala Glu Ala Ala Thr
85 90 95

Gly Trp Gln Thr Ile Asp Gly Lys Lys Tyr Tyr Phe Asn Thr Asn Thr
100 105 110

Phe Ile Ala Ser Thr Gly Tyr Thr Ser Ile Asn Gly Lys His Phe Tyr
115 120 125

Phe Asn Thr Asp Gly Ile Met Gln Ile Gly Val Phe Lys Gly Pro Asn
130 135 140

Gly Phe Glu Tyr Phe Ala Pro Ala Asn Thr Asp Ala Asn Asn Ile Glu
145 150 155 160

Gly Gln Ala Ile Leu Tyr Gln Asn Lys Phe Leu Thr Leu Asn Gly Lys
165 170 175

Lys Tyr Tyr Phe Gly Ser Asp Ser Lys Ala Val Thr Gly Leu Arg Thr
180 185 190

Ile Asp Gly Lys Lys Tyr Tyr Phe Asn Thr Asn Thr Ala Val Ala Val
195 200 205

Thr Gly Trp Gln Thr Ile Asn Gly Lys Lys Tyr Tyr Phe Asn Thr Asn
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Thr Ser Ile Ala Ser Thr Gly Tyr Thr Ile Ile Ser Gly Lys His Phe

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<213> Artificial Sequence

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<223> Q-Toxin fusion protein

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<222> (588)..(588)
<223> Xaa can be any naturally occurring amino acid

<400> 21

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Tyr Tyr Phe Thr Asp Glu His Phe Lys Asp Leu Lys Leu Met Ala Pro
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Ile Lys Asp Gly Asn Leu Lys Phe Glu Glu Lys Lys Val Asp Lys Leu
35 40 45

Leu Asp Lys Asp Lys Ser Asp Val Lys Ser Ile Arg Trp Thr Gly Arg
50 55 60

Ile Ile Pro Ser Lys Asp Gly Glu Tyr Thr Leu Ser Thr Asp Arg Asp
65 70 75 80

Asp Val Leu Met Gln Val Asn Thr Glu Ser Thr Ile Ser Asn Thr Leu
85 90 95

Lys Val Asn Met Lys Lys Gly Lys Glu Tyr Lys Val Arg Ile Glu Leu
100 105 110

Gln Asp Lys Asn Leu Gly Ser Ile Asp Asn Leu Ser Ser Pro Asn Leu
115 120 125

Tyr Trp Glu Leu Asp Gly Met Lys Lys Ile Ile Pro Glu Glu Asn Leu
130 135 140

Phe Leu Arg Asp Tyr Ser Asn Ile Glu Lys Asp Asp Pro Phe Ile Pro

145		150		155		160									
Asn	Asn	Asn	Phe	Phe	Asp	Pro	Lys	Leu	Met	Ser	Asp	Trp	Glu	Asp	Glu
			165					170						175	
Asp	Leu	Asp	Thr	Asp	Asn	Asp	Asn	Ile	Pro	Asp	Ser	Tyr	Glu	Arg	Asn
			180					185					190		
Gly	Tyr	Thr	Ile	Lys	Asp	Leu	Ile	Ala	Val	Lys	Trp	Glu	Asp	Ser	Phe
		195					200					205			
Ala	Glu	Gln	Gly	Tyr	Lys	Lys	Tyr	Val	Ser	Asn	Tyr	Leu	Glu	Ser	Asn
	210					215					220				
Thr	Ala	Gly	Asp	Pro	Tyr	Thr	Asp	Tyr	Glu	Lys	Ala	Ser	Gly	Ser	Phe
225					230					235					240
Asp	Lys	Ala	Ile	Lys	Thr	Glu	Ala	Arg	Asp	Pro	Leu	Val	Ala	Ala	Tyr
				245					250					255	
Pro	Ile	Val	Gly	Val	Gly	Met	Glu	Lys	Leu	Ile	Ile	Ser	Thr	Asn	Glu
			260					265					270		
His	Ala	Ser	Thr	Asp	Gln	Gly	Lys	Thr	Val	Ser	Arg	Ala	Thr	Thr	Asn
	275						280					285			
Ser	Lys	Thr	Glu	Ser	Asn	Thr	Ala	Gly	Val	Ser	Val	Asn	Val	Gly	Tyr
	290					295					300				
Gln	Asn	Gly	Phe	Thr	Ala	Asn	Val	Thr	Thr	Asn	Tyr	Ser	His	Thr	Thr
305					310					315					320
Asp	Asn	Ser	Thr	Ala	Val	Gln	Asp	Ser	Asn	Gly	Glu	Ser	Trp	Asn	Thr
				325					330					335	
Gly	Leu	Ser	Ile	Asn	Lys	Gly	Glu	Ser	Ala	Tyr	Ile	Asn	Ala	Asn	Val
			340					345					350		
Arg	Tyr	Tyr	Asn	Thr	Gly	Thr	Ala	Pro	Met	Tyr	Lys	Val	Thr	Pro	Thr
		355					360					365			

Thr Asn Leu Val Leu Asp Gly Asp Thr Leu Ser Thr Ile Lys Ala Gln
370 375 380

Glu Asn Gln Ile Gly Asn Asn Leu Ser Pro Gly Asp Thr Tyr Pro Lys
385 390 395 400

Lys Gly Leu Ser Pro Leu Ala Leu Asn Thr Met Asp Gln Phe Ser Ser
405 410 415

Arg Leu Ile Pro Ile Asn Tyr Asp Gln Leu Lys Lys Leu Asp Ala Gly
420 425 430

Lys Gln Ile Lys Leu Glu Thr Thr Gln Val Ser Gly Asn Phe Gly Thr
435 440 445

Lys Asn Ser Ser Gly Gln Ile Val Thr Glu Gly Asn Ser Trp Ser Asp
450 455 460

Tyr Ile Ser Gln Ile Asp Ser Ile Ser Ala Ser Ile Ile Leu Asp Thr
465 470 475 480

Glu Asn Glu Ser Tyr Glu Arg Arg Val Thr Ala Lys Asn Leu Gln Asp
485 490 495

Pro Glu Asp Lys Thr Pro Glu Leu Thr Ile Gly Glu Ala Ile Glu Lys
500 505 510

Ala Phe Gly Ala Thr Lys Lys Asp Gly Leu Leu Tyr Phe Asn Asp Ile
515 520 525

Pro Ile Asp Glu Ser Cys Val Glu Leu Ile Phe Asp Asp Asn Thr Ala
530 535 540

Asn Lys Ile Lys Asp Ser Leu Lys Thr Leu Ser Asp Lys Lys Ile Tyr
545 550 555 560

Asn Val Lys Leu Glu Arg Gly Met Asn Ile Leu Ile Lys Thr Pro Thr
565 570 575

Tyr Phe Thr Asn Phe Asp Asp Tyr Asn Asn Tyr Xaa Ser Thr Trp Ser

580

585

590

Asn Val Asn Thr Thr Asn Gln Asp Gly Leu Gln Gly Ser Ala Asn Lys
 595 600 605

Leu Asn Gly Glu Thr Lys Ile Lys Ile Pro Met Ser Glu Leu Lys Pro
 610 615 620

Tyr Lys Arg Tyr Val Phe Ser Gly Tyr Ser Lys Asp Pro Leu Thr Ser
 625 630 635 640

Asn Ser Ile Ile Val Lys Ile Lys Ala Lys Glu Glu Lys Thr Asp Tyr
 645 650 655

Leu Val Pro Glu Gln Gly Tyr Thr Lys Phe Ser Tyr Glu Phe Glu Thr
 660 665 670

Thr Glu Lys Asp Ser Ser Asn Ile Glu Ile Thr Leu Ile Gly Ser Gly
 675 680 685

Thr Thr Tyr Leu Asp Asn Leu Ser Ile Thr Glu Leu Asn Ser Thr Pro
 690 695 700

Glu Ile Leu Asp Glu Pro Glu Val Lys Ile Pro Thr Asp Gln Glu Ile
 705 710 715 720

Met Asp Ala His Lys Ile Tyr Phe Ala Asp Leu Asn Phe Asn Pro Ser
 725 730 735

Thr Gly Asn Thr Tyr Ile Asn Gly Met Tyr Phe Ala Pro Thr Gln Thr
 740 745 750

Asn Lys Glu Ala Leu Asp Tyr Ile Gln Lys Tyr Arg Val Glu Ala Thr
 755 760 765

Leu Gln Tyr Ser Gly Phe Lys Asp Ile Gly Thr Lys Asp Lys Glu Met
 770 775 780

Arg Asn Tyr Leu Gly Asp Pro Asn Gln Pro Lys Thr Asn Tyr Val Asn
 785 790 795 800

Leu Arg Ser Tyr Phe Thr Gly Gly Glu Asn Ile Met Thr Tyr Lys Lys
805 810 815

Leu Arg Ile Tyr Ala Ile Thr Pro Asp Asp Arg Glu Leu Leu Val Leu
820 825 830

Ser Val Asp Ala Ser Met Val Ser Gly Leu Ile Tyr Ile Asn Asp Ser
835 840 845

Leu Tyr Tyr Phe Lys Pro Pro Val Asn Asn Leu Ile Thr Gly Phe Val
850 855 860

Thr Val Gly Asp Asp Lys Tyr Tyr Phe Asn Pro Ile Asn Gly Gly Ala
865 870 875 880

Ala Ser Ile Gly Glu Thr Ile Ile Asp Asp Lys Asn Tyr Tyr Phe Asn
885 890 895

Gln Ser Gly Val Leu Gln Thr Gly Val Phe Ser Thr Glu Asp Gly Phe
900 905 910

Lys Tyr Phe Ala Pro Ala Asn Thr Leu Asp Glu Asn Leu Glu Gly Glu
915 920 925

Ala Ile Asp Phe Thr Gly Lys Leu Ile Ile Asp Glu Asn Ile Tyr Tyr
930 935 940

Phe Asp Asp Asn Tyr Arg Gly Ala Val Glu Trp Lys Glu Leu Asp Gly
945 950 955 960

Glu Met His Tyr Phe Ser Pro Glu Thr Gly Lys Ala Phe Lys Gly Leu
965 970 975

Asn Gln Ile Gly Asp Tyr Lys Tyr Tyr Phe Asn Ser Asp Gly Val Met
980 985 990

Gln Lys Gly Phe Val Ser Ile Asn Asp Asn Lys His Tyr Phe Asp Asp
995 1000 1005

Ser Gly Val Met Lys Val Gly Tyr Thr Glu Ile Asp Gly Lys His

1010	1015	1020
Phe Tyr Phe Ala Glu Asn Gly 1025 1030	Glu Met Gln Ile Gly 1035	Val Phe Asn
Thr Glu Asp Gly Phe Lys Tyr 1040 1045	Phe Ala His His Asn 1050	Glu Asp Leu
Gly Asn Glu Glu Gly Glu Glu 1055 1060	Ile Ser Tyr Ser Gly 1065	Ile Leu Asn
Phe Asn Asn Lys Ile Tyr Tyr 1070 1075	Phe Asp Asp Ser Phe 1080	Thr Ala Val
Val Gly Trp Lys Asp Leu Glu 1085 1090	Asp Gly Ser Lys Tyr 1095	Tyr Phe Asp
Glu Asp Thr Ala Glu Ala Tyr 1100 1105	Ile Gly Leu Ser Leu 1110	Ile Asn Asp
Gly Gln Tyr Tyr Phe Asn Asp 1115 1120	Asp Gly Ile Met Gln 1125	Val Gly Phe
Val Thr Ile Asn Asp Lys Val 1130 1135	Phe Tyr Phe Ser Asp 1140	Ser Gly Ile
Ile Glu Ser Gly Val Gln Asn 1145 1150	Ile Asp Asp Asn Tyr 1155	Phe Tyr Ile
Asp Asp Asn Gly Ile Val Gln 1160 1165	Ile Gly Val Phe Asp 1170	Thr Ser Asp
Gly Tyr Lys Tyr Phe Ala Pro 1175 1180	Ala Asn Thr Val Asn 1185	Asp Asn Ile
Tyr Gly Gln Ala Val Glu Tyr 1190 1195	Ser Gly Leu Val Arg 1200	Val Gly Glu
Asp Val Tyr Tyr Phe Gly Glu 1205 1210	Thr Tyr Thr Ile Glu 1215	Thr Gly Trp

Ile Tyr Asp Met Glu Asn Glu Ser Asp Lys Tyr Tyr Phe Asn Pro
1220 1225 1230

Glu Thr Lys Lys Ala Cys Lys Gly Ile Asn Leu Ile Asp Asp Ile
1235 1240 1245

Lys Tyr Tyr Phe Asp Glu Lys Gly Ile Met Arg Thr Gly Leu Ile
1250 1255 1260

Ser Phe Glu Asn Asn Asn Tyr Tyr Phe Asn Glu Asn Gly Glu Met
1265 1270 1275

Gln Phe Gly Tyr Ile Asn Ile Glu Asp Lys Met Phe Tyr Phe Gly
1280 1285 1290

Glu Asp Gly Val Met Gln Ile Gly Val Phe Asn Thr Pro Asp Gly
1295 1300 1305

Phe Lys Tyr Phe Ala His Gln Asn Thr Leu Asp Glu Asn Phe Glu
1310 1315 1320

Gly Glu Ser Ile Asn Tyr Thr Gly Trp Leu Asp Leu Asp Glu Lys
1325 1330 1335

Arg Tyr Tyr Phe Thr Asp Glu Tyr Ile Ala Ala Thr Gly Ser Val
1340 1345 1350

Ile Ile Asp Gly Glu Glu Tyr Tyr Phe Asp Pro Asp Thr Ala Gln
1355 1360 1365

Leu Val Ile Ser Glu Ser Arg Met Val Thr Gly Val Phe Lys Gly
1370 1375 1380

Pro Asn Gly Phe Glu Tyr Phe Ala Pro Ala Asn Thr His Asn Asn
1385 1390 1395

Asn Ile Glu Gly Gln Ala Ile Val Tyr Gln Asn Lys Phe Leu Thr
1400 1405 1410

Leu Asn Gly Lys Lys Tyr Tyr Phe Asp Asn Asp Ser Lys Ala Val

1415						1420						1425			
Thr	Gly	Trp	Gln	Thr	Ile	Asp	Gly	Lys	Lys	Tyr	Tyr	Phe	Asn	Leu	
1430						1435					1440				
Asn	Thr	Ala	Glu	Ala	Ala	Thr	Gly	Trp	Gln	Thr	Ile	Asp	Gly	Lys	
1445						1450					1455				
Lys	Tyr	Tyr	Phe	Asn	Leu	Asn	Thr	Ala	Glu	Ala	Ala	Thr	Gly	Trp	
1460						1465					1470				
Gln	Thr	Ile	Asp	Gly	Lys	Lys	Tyr	Tyr	Phe	Asn	Thr	Asn	Thr	Phe	
1475						1480					1485				
Ile	Ala	Ser	Thr	Gly	Tyr	Thr	Ser	Ile	Asn	Gly	Lys	His	Phe	Tyr	
1490						1495					1500				
Phe	Asn	Thr	Asp	Gly	Ile	Met	Gln	Ile	Gly	Val	Phe	Lys	Gly	Pro	
1505						1510					1515				
Asn	Gly	Phe	Glu	Tyr	Phe	Ala	Pro	Ala	Asn	Thr	Asp	Ala	Asn	Asn	
1520						1525					1530				
Ile	Glu	Gly	Gln	Ala	Ile	Leu	Tyr	Gln	Asn	Lys	Phe	Leu	Thr	Leu	
1535						1540					1545				
Asn	Gly	Lys	Lys	Tyr	Tyr	Phe	Gly	Ser	Asp	Ser	Lys	Ala	Val	Thr	
1550						1555					1560				
Gly	Leu	Arg	Thr	Ile	Asp	Gly	Lys	Lys	Tyr	Tyr	Phe	Asn	Thr	Asn	
1565						1570					1575				
Thr	Ala	Val	Ala	Val	Thr	Gly	Trp	Gln	Thr	Ile	Asn	Gly	Lys	Lys	
1580						1585					1590				
Tyr	Tyr	Phe	Asn	Thr	Asn	Thr	Ser	Ile	Ala	Ser	Thr	Gly	Tyr	Thr	
1595						1600					1605				
Ile	Ile	Ser	Gly	Lys	His	Phe	Tyr	Phe	Asn	Thr	Asp	Gly	Ile	Met	
1610						1615					1620				

Gln Ile Gly Val Phe Lys Gly Pro Asp Gly Phe Glu Tyr Phe Ala
1625 1630 1635

Pro Ala Asn Thr Asp Ala Asn Asn Ile Glu Gly Gln Ala Ile Arg
1640 1645 1650

Tyr Gln Asn Arg Phe Leu Tyr Leu His Asp Asn Ile Tyr Tyr Phe
1655 1660 1665

Gly Asn Asn Ser Lys Ala Ala Thr Gly Trp Val Thr Ile Asp Gly
1670 1675 1680

Asn Arg Tyr Tyr Phe Glu Pro Asn Thr Ala Met Gly Ala Asn Gly
1685 1690 1695

Tyr Lys Thr Ile Asp Asn Lys Asn Phe Tyr Phe Arg Asn Gly Leu
1700 1705 1710

Pro Gln Ile Gly Val Phe Lys Gly Ser Asn Gly Phe Glu Tyr Phe
1715 1720 1725

Ala Pro Ala Asn Thr Asp Ala Asn Asn Ile Glu Gly Gln Ala Ile
1730 1735 1740

Arg Tyr Gln Asn Arg Phe Leu His Leu Leu Gly Lys Ile Tyr Tyr
1745 1750 1755

Phe Gly Asn Asn Ser Lys Ala Val Thr Gly Trp Gln Thr Ile Asn
1760 1765 1770

Gly Lys Val Tyr Tyr Phe Met Pro Asp Thr Ala Met Ala Ala Ala
1775 1780 1785

Gly Gly Leu Phe Glu Ile Asp Gly Val Ile Tyr Phe Phe Gly Val
1790 1795 1800

Asp Gly Val Lys Ala Pro Gly Ile Tyr Gly Thr Ser Met Val Ser
1805 1810 1815

Gly Leu Ile Tyr Ile Asn Asp Ser Leu Tyr Tyr Phe Lys Pro Pro

1820						1825					1830			
Val	Asn	Asn	Leu	Ile	Thr	Gly	Phe	Val	Thr	Val	Gly	Asp	Asp	Lys
1835						1840					1845			
Tyr	Tyr	Phe	Asn	Pro	Ile	Asn	Gly	Gly	Ala	Ala	Ser	Ile	Gly	Glu
1850						1855					1860			
Thr	Ile	Ile	Asp	Asp	Lys	Asn	Tyr	Tyr	Phe	Asn	Gln	Ser	Gly	Val
1865						1870					1875			
Leu	Gln	Thr	Gly	Val	Phe	Ser	Thr	Glu	Asp	Gly	Phe	Lys	Tyr	Phe
1880						1885					1890			
Ala	Pro	Ala	Asn	Thr	Leu	Asp	Glu	Asn	Leu	Glu	Gly	Glu	Ala	Ile
1895						1900					1905			
Asp	Phe	Thr	Gly	Lys	Leu	Ile	Ile	Asp	Glu	Asn	Ile	Tyr	Tyr	Phe
1910						1915					1920			
Asp	Asp	Asn	Tyr	Arg	Gly	Ala	Val	Glu	Trp	Lys	Glu	Leu	Asp	Gly
1925						1930					1935			
Glu	Met	His	Tyr	Phe	Ser	Pro	Glu	Thr	Gly	Lys	Ala	Phe	Lys	Gly
1940						1945					1950			
Leu	Asn	Gln	Ile	Gly	Asp	Tyr	Lys	Tyr	Tyr	Phe	Asn	Ser	Asp	Gly
1955						1960					1965			
Val	Met	Gln	Lys	Gly	Phe	Val	Ser	Ile	Asn	Asp	Asn	Lys	His	Tyr
1970						1975					1980			
Phe	Asp	Asp	Ser	Gly	Val	Met	Lys	Val	Gly	Tyr	Thr	Glu	Ile	Asp
1985						1990					1995			
Gly	Lys	His	Phe	Tyr	Phe	Ala	Glu	Asn	Gly	Glu	Met	Gln	Ile	Gly
2000						2005					2010			
Val	Phe	Asn	Thr	Glu	Asp	Gly	Phe	Lys	Tyr	Phe	Ala	His	His	Asn
2015						2020					2025			

Glu Asp Leu Gly Asn Glu Glu Gly Glu Glu Ile Ser Tyr Ser Gly
2030 2035 2040

Ile Leu Asn Phe Asn Asn Lys Ile Tyr Tyr Phe Asp Asp Ser Phe
2045 2050 2055

Thr Ala Val Val Gly Trp Lys Asp Leu Glu Asp Gly Ser Lys Tyr
2060 2065 2070

Tyr Phe Asp Glu Asp Thr Ala Glu Ala Tyr Ile Gly Leu Ser Leu
2075 2080 2085

Ile Asn Asp Gly Gln Tyr Tyr Phe Asn Asp Asp Gly Ile Met Gln
2090 2095 2100

Val Gly Phe Val Thr Ile Asn Asp Lys Val Phe Tyr Phe Ser Asp
2105 2110 2115

Ser Gly Ile Ile Glu Ser Gly Val Gln Asn Ile Asp Asp Asn Tyr
2120 2125 2130

Phe Tyr Ile Asp Asp Asn Gly Ile Val Gln Ile Gly Val Phe Asp
2135 2140 2145

Thr Ser Asp Gly Tyr Lys Tyr Phe Ala Pro Ala Asn Thr Val Asn
2150 2155 2160

Asp Asn Ile Tyr Gly Gln Ala Val Glu Tyr Ser Gly Leu Val Arg
2165 2170 2175

Val Gly Glu Asp Val Tyr Tyr Phe Gly Glu Thr Tyr Thr Ile Glu
2180 2185 2190

Thr Gly Trp Ile Tyr Asp Met Glu Asn Glu Ser Asp Lys Tyr Tyr
2195 2200 2205

Phe Asn Pro Glu Thr Lys Lys Ala Cys Lys Gly Ile Asn Leu Ile
2210 2215 2220

Asp Asp Ile Lys Tyr Tyr Phe Asp Glu Lys Gly Ile Met Arg Thr

2225

2230

2235

Gly Leu Ile Ser Phe Glu Asn Asn Asn Tyr Tyr Phe Asn Glu Asn
 2240 2245 2250

Gly Glu Met Gln Phe Gly Tyr Ile Asn Ile Glu Asp Lys Met Phe
 2255 2260 2265

Tyr Phe Gly Glu Asp Gly Val Met Gln Ile Gly Val Phe Asn Thr
 2270 2275 2280

Pro Asp Gly Phe Lys Tyr Phe Ala His Gln Asn Thr Leu Asp Glu
 2285 2290 2295

Asn Phe Glu Gly Glu Ser Ile Asn Tyr Thr Gly Trp Leu Asp Leu
 2300 2305 2310

Asp Glu Lys Arg Tyr Tyr Phe Thr Asp Glu Tyr Ile Ala Ala Thr
 2315 2320 2325

Gly Ser Val Ile Ile Asp Gly Glu Glu Tyr Tyr Phe Asp Pro Asp
 2330 2335 2340

Thr Ala Gln Leu Val Ile Ser Glu
 2345 2350

<210> 22
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 <213> Clostridium difficile

<220>
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 <222> (588)..(588)
 <223> Xaa can be any naturally occurring amino acid

<400> 22

Met Glu Ile Val Asn Glu Asp Ile Leu Pro Asn Asn Gly Leu Met Gly
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Tyr Tyr Phe Thr Asp Glu His Phe Lys Asp Leu Lys Leu Met Ala Pro
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Ile Lys Asp Gly Asn Leu Lys Phe Glu Glu Lys Lys Val Asp Lys Leu
35 40 45

Leu Asp Lys Asp Lys Ser Asp Val Lys Ser Ile Arg Trp Thr Gly Arg
50 55 60

Ile Ile Pro Ser Lys Asp Gly Glu Tyr Thr Leu Ser Thr Asp Arg Asp
65 70 75 80

Asp Val Leu Met Gln Val Asn Thr Glu Ser Thr Ile Ser Asn Thr Leu
85 90 95

Lys Val Asn Met Lys Lys Gly Lys Glu Tyr Lys Val Arg Ile Glu Leu
100 105 110

Gln Asp Lys Asn Leu Gly Ser Ile Asp Asn Leu Ser Ser Pro Asn Leu
115 120 125

Tyr Trp Glu Leu Asp Gly Met Lys Lys Ile Ile Pro Glu Glu Asn Leu
130 135 140

Phe Leu Arg Asp Tyr Ser Asn Ile Glu Lys Asp Asp Pro Phe Ile Pro
145 150 155 160

Asn Asn Asn Phe Phe Asp Pro Lys Leu Met Ser Asp Trp Glu Asp Glu
165 170 175

Asp Leu Asp Thr Asp Asn Asp Asn Ile Pro Asp Ser Tyr Glu Arg Asn
180 185 190

Gly Tyr Thr Ile Lys Asp Leu Ile Ala Val Lys Trp Glu Asp Ser Phe
195 200 205

Ala Glu Gln Gly Tyr Lys Lys Tyr Val Ser Asn Tyr Leu Glu Ser Asn
210 215 220

Thr Ala Gly Asp Pro Tyr Thr Asp Tyr Glu Lys Ala Ser Gly Ser Phe
225 230 235 240

Asp Lys Ala Ile Lys Thr Glu Ala Arg Asp Pro Leu Val Ala Ala Tyr
245 250 255

Pro Ile Val Gly Val Gly Met Glu Lys Leu Ile Ile Ser Thr Asn Glu
260 265 270

His Ala Ser Thr Asp Gln Gly Lys Thr Val Ser Arg Ala Thr Thr Asn
275 280 285

Ser Lys Thr Glu Ser Asn Thr Ala Gly Val Ser Val Asn Val Gly Tyr
290 295 300

Gln Asn Gly Phe Thr Ala Asn Val Thr Thr Asn Tyr Ser His Thr Thr
305 310 315 320

Asp Asn Ser Thr Ala Val Gln Asp Ser Asn Gly Glu Ser Trp Asn Thr
325 330 335

Gly Leu Ser Ile Asn Lys Gly Glu Ser Ala Tyr Ile Asn Ala Asn Val
340 345 350

Arg Tyr Tyr Asn Thr Gly Thr Ala Pro Met Tyr Lys Val Thr Pro Thr
355 360 365

Thr Asn Leu Val Leu Asp Gly Asp Thr Leu Ser Thr Ile Lys Ala Gln
370 375 380

Glu Asn Gln Ile Gly Asn Asn Leu Ser Pro Gly Asp Thr Tyr Pro Lys
385 390 395 400

Lys Gly Leu Ser Pro Leu Ala Leu Asn Thr Met Asp Gln Phe Ser Ser
405 410 415

Arg Leu Ile Pro Ile Asn Tyr Asp Gln Leu Lys Lys Leu Asp Ala Gly
420 425 430

Lys Gln Ile Lys Leu Glu Thr Thr Gln Val Ser Gly Asn Phe Gly Thr
435 440 445

Lys Asn Ser Ser Gly Gln Ile Val Thr Glu Gly Asn Ser Trp Ser Asp
450 455 460

Tyr Ile Ser Gln Ile Asp Ser Ile Ser Ala Ser Ile Ile Leu Asp Thr
465 470 475 480

Glu Asn Glu Ser Tyr Glu Arg Arg Val Thr Ala Lys Asn Leu Gln Asp
485 490 495

Pro Glu Asp Lys Thr Pro Glu Leu Thr Ile Gly Glu Ala Ile Glu Lys
500 505 510

Ala Phe Gly Ala Thr Lys Lys Asp Gly Leu Leu Tyr Phe Asn Asp Ile
515 520 525

Pro Ile Asp Glu Ser Cys Val Glu Leu Ile Phe Asp Asp Asn Thr Ala
530 535 540

Asn Lys Ile Lys Asp Ser Leu Lys Thr Leu Ser Asp Lys Lys Ile Tyr
545 550 555 560

Asn Val Lys Leu Glu Arg Gly Met Asn Ile Leu Ile Lys Thr Pro Thr
565 570 575

Tyr Phe Thr Asn Phe Asp Asp Tyr Asn Asn Tyr Xaa Ser Thr Trp Ser
580 585 590

Asn Val Asn Thr Thr Asn Gln Asp Gly Leu Gln Gly Ser Ala Asn Lys
595 600 605

Leu Asn Gly Glu Thr Lys Ile Lys Ile Pro Met Ser Glu Leu Lys Pro
610 615 620

Tyr Lys Arg Tyr Val Phe Ser Gly Tyr Ser Lys Asp Pro Leu Thr Ser
625 630 635 640

Asn Ser Ile Ile Val Lys Ile Lys Ala Lys Glu Glu Lys Thr Asp Tyr
645 650 655

Leu Val Pro Glu Gln Gly Tyr Thr Lys Phe Ser Tyr Glu Phe Glu Thr
660 665 670

Thr Glu Lys Asp Ser Ser Asn Ile Glu Ile Thr Leu Ile Gly Ser Gly
675 680 685

Thr Thr Tyr Leu Asp Asn Leu Ser Ile Thr Glu Leu Asn Ser Thr Pro
690 695 700

Glu Ile Leu Asp Glu Pro Glu Val Lys Ile Pro Thr Asp Gln Glu Ile
705 710 715 720

Met Asp Ala His Lys Ile Tyr Phe Ala Asp Leu Asn Phe Asn Pro Ser
725 730 735

Thr Gly Asn Thr Tyr Ile Asn Gly Met Tyr Phe Ala Pro Thr Gln Thr
740 745 750

Asn Lys Glu Ala Leu Asp Tyr Ile Gln Lys Tyr Arg Val Glu Ala Thr
755 760 765

Leu Gln Tyr Ser Gly Phe Lys Asp Ile Gly Thr Lys Asp Lys Glu Met
770 775 780

Arg Asn Tyr Leu Gly Asp Pro Asn Gln Pro Lys Thr Asn Tyr Val Asn
785 790 795 800

Leu Arg Ser Tyr Phe Thr Gly Gly Glu Asn Ile Met Thr Tyr Lys Lys
805 810 815

Leu Arg Ile Tyr Ala Ile Thr Pro Asp Asp Arg Glu Leu Leu Val Leu
820 825 830

Ser Val Asp
835

<210> 23
<211> 536
<212> PRT
<213> Clostridium difficile

<400> 23

Met Val Ser Gly Leu Ile Tyr Ile Asn Asp Ser Leu Tyr Tyr Phe Lys
1 5 10 15

Pro Pro Val Asn Asn Leu Ile Thr Gly Phe Val Thr Val Gly Asp Asp
20 25 30

Lys Tyr Tyr Phe Asn Pro Ile Asn Gly Gly Ala Ala Ser Ile Gly Glu
35 40 45

Thr Ile Ile Asp Asp Lys Asn Tyr Tyr Phe Asn Gln Ser Gly Val Leu
50 55 60

Gln Thr Gly Val Phe Ser Thr Glu Asp Gly Phe Lys Tyr Phe Ala Pro
65 70 75 80

Ala Asn Thr Leu Asp Glu Asn Leu Glu Gly Glu Ala Ile Asp Phe Thr
85 90 95

Gly Lys Leu Ile Ile Asp Glu Asn Ile Tyr Tyr Phe Asp Asp Asn Tyr
100 105 110

Arg Gly Ala Val Glu Trp Lys Glu Leu Asp Gly Glu Met His Tyr Phe
115 120 125

Ser Pro Glu Thr Gly Lys Ala Phe Lys Gly Leu Asn Gln Ile Gly Asp
130 135 140

Tyr Lys Tyr Tyr Phe Asn Ser Asp Gly Val Met Gln Lys Gly Phe Val
145 150 155 160

Ser Ile Asn Asp Asn Lys His Tyr Phe Asp Asp Ser Gly Val Met Lys
165 170 175

Val Gly Tyr Thr Glu Ile Asp Gly Lys His Phe Tyr Phe Ala Glu Asn
180 185 190

Gly Glu Met Gln Ile Gly Val Phe Asn Thr Glu Asp Gly Phe Lys Tyr
195 200 205

Phe Ala His His Asn Glu Asp Leu Gly Asn Glu Glu Gly Glu Glu Ile
210 215 220

Ser Tyr Ser Gly Ile Leu Asn Phe Asn Asn Lys Ile Tyr Tyr Phe Asp

225		230		235		240									
Asp	Ser	Phe	Thr	Ala	Val	Val	Gly	Trp	Lys	Asp	Leu	Glu	Asp	Gly	Ser
				245					250					255	
Lys	Tyr	Tyr	Phe	Asp	Glu	Asp	Thr	Ala	Glu	Ala	Tyr	Ile	Gly	Leu	Ser
			260					265					270		
Leu	Ile	Asn	Asp	Gly	Gln	Tyr	Tyr	Phe	Asn	Asp	Asp	Gly	Ile	Met	Gln
		275					280					285			
Val	Gly	Phe	Val	Thr	Ile	Asn	Asp	Lys	Val	Phe	Tyr	Phe	Ser	Asp	Ser
	290						295				300				
Gly	Ile	Ile	Glu	Ser	Gly	Val	Gln	Asn	Ile	Asp	Asp	Asn	Tyr	Phe	Tyr
305					310					315					320
Ile	Asp	Asp	Asn	Gly	Ile	Val	Gln	Ile	Gly	Val	Phe	Asp	Thr	Ser	Asp
				325					330					335	
Gly	Tyr	Lys	Tyr	Phe	Ala	Pro	Ala	Asn	Thr	Val	Asn	Asp	Asn	Ile	Tyr
			340					345					350		
Gly	Gln	Ala	Val	Glu	Tyr	Ser	Gly	Leu	Val	Arg	Val	Gly	Glu	Asp	Val
		355					360					365			
Tyr	Tyr	Phe	Gly	Glu	Thr	Tyr	Thr	Ile	Glu	Thr	Gly	Trp	Ile	Tyr	Asp
	370					375					380				
Met	Glu	Asn	Glu	Ser	Asp	Lys	Tyr	Tyr	Phe	Asn	Pro	Glu	Thr	Lys	Lys
385					390					395					400
Ala	Cys	Lys	Gly	Ile	Asn	Leu	Ile	Asp	Asp	Ile	Lys	Tyr	Tyr	Phe	Asp
			405						410					415	
Glu	Lys	Gly	Ile	Met	Arg	Thr	Gly	Leu	Ile	Ser	Phe	Glu	Asn	Asn	Asn
			420					425					430		
Tyr	Tyr	Phe	Asn	Glu	Asn	Gly	Glu	Met	Gln	Phe	Gly	Tyr	Ile	Asn	Ile
		435					440					445			

Glu Asp Lys Met Phe Tyr Phe Gly Glu Asp Gly Val Met Gln Ile Gly
450 455 460

Val Phe Asn Thr Pro Asp Gly Phe Lys Tyr Phe Ala His Gln Asn Thr
465 470 475 480

Leu Asp Glu Asn Phe Glu Gly Glu Ser Ile Asn Tyr Thr Gly Trp Leu
485 490 495

Asp Leu Asp Glu Lys Arg Tyr Tyr Phe Thr Asp Glu Tyr Ile Ala Ala
500 505 510

Thr Gly Ser Val Ile Ile Asp Gly Glu Glu Tyr Tyr Phe Asp Pro Asp
515 520 525

Thr Ala Gln Leu Val Ile Ser Glu
530 535

<210> 24
<211> 438
<212> PRT
<213> Clostridium difficile

<400> 24

Met Val Thr Gly Val Phe Lys Gly Pro Asn Gly Phe Glu Tyr Phe Ala
1 5 10 15

Pro Ala Asn Thr His Asn Asn Asn Ile Glu Gly Gln Ala Ile Val Tyr
20 25 30

Gln Asn Lys Phe Leu Thr Leu Asn Gly Lys Lys Tyr Tyr Phe Asp Asn
35 40 45

Asp Ser Lys Ala Val Thr Gly Trp Gln Thr Ile Asp Gly Lys Lys Tyr
50 55 60

Tyr Phe Asn Leu Asn Thr Ala Glu Ala Ala Thr Gly Trp Gln Thr Ile
65 70 75 80

Asp Gly Lys Lys Tyr Tyr Phe Asn Leu Asn Thr Ala Glu Ala Ala Thr
85 90 95

Gly Trp Gln Thr Ile Asp Gly Lys Lys Tyr Tyr Phe Asn Thr Asn Thr
100 105 110

Phe Ile Ala Ser Thr Gly Tyr Thr Ser Ile Asn Gly Lys His Phe Tyr
115 120 125

Phe Asn Thr Asp Gly Ile Met Gln Ile Gly Val Phe Lys Gly Pro Asn
130 135 140

Gly Phe Glu Tyr Phe Ala Pro Ala Asn Thr Asp Ala Asn Asn Ile Glu
145 150 155 160

Gly Gln Ala Ile Leu Tyr Gln Asn Lys Phe Leu Thr Leu Asn Gly Lys
165 170 175

Lys Tyr Tyr Phe Gly Ser Asp Ser Lys Ala Val Thr Gly Leu Arg Thr
180 185 190

Ile Asp Gly Lys Lys Tyr Tyr Phe Asn Thr Asn Thr Ala Val Ala Val
195 200 205

Thr Gly Trp Gln Thr Ile Asn Gly Lys Lys Tyr Tyr Phe Asn Thr Asn
210 215 220

Thr Ser Ile Ala Ser Thr Gly Tyr Thr Ile Ile Ser Gly Lys His Phe
225 230 235 240

Tyr Phe Asn Thr Asp Gly Ile Met Gln Ile Gly Val Phe Lys Gly Pro
245 250 255

Asp Gly Phe Glu Tyr Phe Ala Pro Ala Asn Thr Asp Ala Asn Asn Ile
260 265 270

Glu Gly Gln Ala Ile Arg Tyr Gln Asn Arg Phe Leu Tyr Leu His Asp
275 280 285

Asn Ile Tyr Tyr Phe Gly Asn Asn Ser Lys Ala Ala Thr Gly Trp Val
290 295 300

Thr Ile Asp Gly Asn Arg Tyr Tyr Phe Glu Pro Asn Thr Ala Met Gly
305 310 315 320

Ala Asn Gly Tyr Lys Thr Ile Asp Asn Lys Asn Phe Tyr Phe Arg Asn
325 330 335

Gly Leu Pro Gln Ile Gly Val Phe Lys Gly Ser Asn Gly Phe Glu Tyr
340 345 350

Phe Ala Pro Ala Asn Thr Asp Ala Asn Asn Ile Glu Gly Gln Ala Ile
355 360 365

Arg Tyr Gln Asn Arg Phe Leu His Leu Leu Gly Lys Ile Tyr Tyr Phe
370 375 380

Gly Asn Asn Ser Lys Ala Val Thr Gly Trp Gln Thr Ile Asn Gly Lys
385 390 395 400

Val Tyr Tyr Phe Met Pro Asp Thr Ala Met Ala Ala Ala Gly Gly Leu
405 410 415

Phe Glu Ile Asp Gly Val Ile Tyr Phe Phe Gly Val Asp Gly Val Lys
420 425 430

Ala Pro Gly Ile Tyr Gly
435

<210> 25
<211> 536
<212> PRT
<213> Clostridium difficile

<400> 25

Met Val Ser Gly Leu Ile Tyr Ile Asn Asp Ser Leu Tyr Tyr Phe Lys
1 5 10 15

Pro Pro Val Asn Asn Leu Ile Thr Gly Phe Val Thr Val Gly Asp Asp
20 25 30

Lys Tyr Tyr Phe Asn Pro Ile Asn Gly Gly Ala Ala Ser Ile Gly Glu
35 40 45

Thr Ile Ile Asp Asp Lys Asn Tyr Tyr Phe Asn Gln Ser Gly Val Leu
50 55 60

Gln Thr Gly Val Phe Ser Thr Glu Asp Gly Phe Lys Tyr Phe Ala Pro
65 70 75 80

Ala Asn Thr Leu Asp Glu Asn Leu Glu Gly Glu Ala Ile Asp Phe Thr
85 90 95

Gly Lys Leu Ile Ile Asp Glu Asn Ile Tyr Tyr Phe Asp Asp Asn Tyr
100 105 110

Arg Gly Ala Val Glu Trp Lys Glu Leu Asp Gly Glu Met His Tyr Phe
115 120 125

Ser Pro Glu Thr Gly Lys Ala Phe Lys Gly Leu Asn Gln Ile Gly Asp
130 135 140

Tyr Lys Tyr Tyr Phe Asn Ser Asp Gly Val Met Gln Lys Gly Phe Val
145 150 155 160

Ser Ile Asn Asp Asn Lys His Tyr Phe Asp Asp Ser Gly Val Met Lys
165 170 175

Val Gly Tyr Thr Glu Ile Asp Gly Lys His Phe Tyr Phe Ala Glu Asn
180 185 190

Gly Glu Met Gln Ile Gly Val Phe Asn Thr Glu Asp Gly Phe Lys Tyr
195 200 205

Phe Ala His His Asn Glu Asp Leu Gly Asn Glu Glu Gly Glu Glu Ile
210 215 220

Ser Tyr Ser Gly Ile Leu Asn Phe Asn Asn Lys Ile Tyr Tyr Phe Asp
225 230 235 240

Asp Ser Phe Thr Ala Val Val Gly Trp Lys Asp Leu Glu Asp Gly Ser
245 250 255

Lys Tyr Tyr Phe Asp Glu Asp Thr Ala Glu Ala Tyr Ile Gly Leu Ser

260

265

270

Leu Ile Asn Asp Gly Gln Tyr Tyr Phe Asn Asp Asp Gly Ile Met Gln
 275 280 285

Val Gly Phe Val Thr Ile Asn Asp Lys Val Phe Tyr Phe Ser Asp Ser
 290 295 300

Gly Ile Ile Glu Ser Gly Val Gln Asn Ile Asp Asp Asn Tyr Phe Tyr
 305 310 315 320

Ile Asp Asp Asn Gly Ile Val Gln Ile Gly Val Phe Asp Thr Ser Asp
 325 330 335

Gly Tyr Lys Tyr Phe Ala Pro Ala Asn Thr Val Asn Asp Asn Ile Tyr
 340 345 350

Gly Gln Ala Val Glu Tyr Ser Gly Leu Val Arg Val Gly Glu Asp Val
 355 360 365

Tyr Tyr Phe Gly Glu Thr Tyr Thr Ile Glu Thr Gly Trp Ile Tyr Asp
 370 375 380

Met Glu Asn Glu Ser Asp Lys Tyr Tyr Phe Asn Pro Glu Thr Lys Lys
 385 390 395 400

Ala Cys Lys Gly Ile Asn Leu Ile Asp Asp Ile Lys Tyr Tyr Phe Asp
 405 410 415

Glu Lys Gly Ile Met Arg Thr Gly Leu Ile Ser Phe Glu Asn Asn Asn
 420 425 430

Tyr Tyr Phe Asn Glu Asn Gly Glu Met Gln Phe Gly Tyr Ile Asn Ile
 435 440 445

Glu Asp Lys Met Phe Tyr Phe Gly Glu Asp Gly Val Met Gln Ile Gly
 450 455 460

Val Phe Asn Thr Pro Asp Gly Phe Lys Tyr Phe Ala His Gln Asn Thr
 465 470 475 480

Leu Asp Glu Asn Phe Glu Gly Glu Ser Ile Asn Tyr Thr Gly Trp Leu
485 490 495

Asp Leu Asp Glu Lys Arg Tyr Tyr Phe Thr Asp Glu Tyr Ile Ala Ala
500 505 510

Thr Gly Ser Val Ile Ile Asp Gly Glu Glu Tyr Tyr Phe Asp Pro Asp
515 520 525

Thr Ala Gln Leu Val Ile Ser Glu
530 535

<210> 26
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically synthesized peptide linker

<400> 26

Gly Gly Gly Gly
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<210> 27
<211> 8
<212> PRT
<213> Unknown

<220>
<223> furin cleavage site sequence

<400> 27

Arg Ala Arg Arg Arg Lys Lys Arg
1 5

<210> 28
<211> 24
<212> DNA
<213> Unknown

<220>
<223> furin cleavage site sequence

<400> 28

cgcgctgcc gccgcaagaa gcgc

24